STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 140623

TO: Janet Epps-Ford
Location: REM-2C05/2C18
Art Unit: 1635
Thursday, December 16, 2004
Case Serial Number: 08/901612

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Epps-Ford,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

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Schulwitz, Paul

From: Epps-Ford, Janet
Sent: Tuesday, December 14, 2004 2:36 PM
To: Schulwitz, Paul
Subject: Question regarding 08/901612...

Applicants in this case have amended the claims to add new sequence identifiers. The newly added sequences are variants of sequences already in the claims for example: original SEQ ID NO: 7 in the claim has the sequence agagatgattaggcagaggt

newly added SEQ ID NO: 58 in the claim has the sequence agagatgauuaggcagaggt.

SEQ ID NO: 58 definitely has a similar structure as SEQ ID NO: 7, would the search for SEQ ID NO: 7 pick up hits that read on SEQ ID NO: 58?

Thanks,
Janet L. Epps-Ford, Ph.D.
Art Unit 1635
Mailbox: Remsen 2C18
Office: Remsen 2C05
Phone: 571-272-0757
Fax: 571-273-0757

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 15, 2004, 09:10:16 ; Search time 764 Seconds
(without alignments)
1237.950 Million cell updates/sec

Title: US-08-901-612A-7
Perfect score: 20
Sequence: 1 agagatgattaggcagaggt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	6	AR027809	AR027809 Sequence
c	2	20	100.0	27	6	AX147024	AX147024 Sequence
	3	20	100.0	30	6	AR027810	AR027810 Sequence
	4	20	100.0	30	6	AR027840	AR027840 Sequence
c	5	20	100.0	87	6	AX151115	AX151115 Sequence
c	6	20	100.0	93	14	HPBPRECAA	D30625 Hepatitis B
c	7	20	100.0	99	14	HPBPRECA	M76687 Hepatitis B
c	8	20	100.0	99	14	HPBPRECB	M76688 Hepatitis B
c	9	20	100.0	99	14	HPBPRECC	M76689 Hepatitis B
c	10	20	100.0	99	14	HPBPRECD	M76690 Hepatitis B
c	11	20	100.0	99	14	HPBPRECE	M76691 Hepatitis B
c	12	20	100.0	99	14	HPBPRECF	M76692 Hepatitis B
c	13	20	100.0	99	14	HPBPRECG	M76693 Hepatitis B
c	14	20	100.0	99	14	HPBPRECH	M76694 Hepatitis B
c	15	20	100.0	99	14	HPBPRECI	M76695 Hepatitis B
c	16	20	100.0	99	14	HPBPRECK	M76697 Hepatitis B
c	17	20	100.0	99	14	HPBPRECL	M76698 Hepatitis B
c	18	20	100.0	99	14	HPBPRECM	M76699 Hepatitis B
c	19	20	100.0	129	6	AX151114	AX151114 Sequence
c	20	20	100.0	150	14	AF528205	AF528205 Hepatitis
c	21	20	100.0	150	14	AF528206	AF528206 Hepatitis
c	22	20	100.0	150	14	AF528207	AF528207 Hepatitis
c	23	20	100.0	150	14	AF528208	AF528208 Hepatitis
c	24	20	100.0	150	14	AF528209	AF528209 Hepatitis
c	25	20	100.0	150	14	AF528210	AF528210 Hepatitis
c	26	20	100.0	150	14	AF528211	AF528211 Hepatitis
c	27	20	100.0	150	14	AF528212	AF528212 Hepatitis
c	28	20	100.0	150	14	AF528213	AF528213 Hepatitis
c	29	20	100.0	150	14	AF528214	AF528214 Hepatitis
c	30	20	100.0	150	14	AF528215	AF528215 Hepatitis
c	31	20	100.0	150	14	AF528216	AF528216 Hepatitis
c	32	20	100.0	150	14	AF528217	AF528217 Hepatitis
c	33	20	100.0	150	14	AF528218	AF528218 Hepatitis
c	34	20	100.0	150	14	AF528219	AF528219 Hepatitis
c	35	20	100.0	150	14	AF528220	AF528220 Hepatitis
c	36	20	100.0	150	14	AF528221	AF528221 Hepatitis
c	37	20	100.0	150	14	AF528222	AF528222 Hepatitis
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c	41	20	100.0	150	14	AF528227	AF528227 Hepatitis
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c	45	20	100.0	150	14	AF528232	AF528232 Hepatitis
c	46	20	100.0	150	14	AF528233	AF528233 Hepatitis
c	47	20	100.0	150	14	AF528234	AF528234 Hepatitis
c	48	20	100.0	150	14	AF528235	AF528235 Hepatitis
c	49	20	100.0	150	14	AF528236	AF528236 Hepatitis
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c	51	20	100.0	150	14	AF528238	AF528238 Hepatitis
c	52	20	100.0	150	14	AF528239	AF528239 Hepatitis
c	53	20	100.0	150	14	AF528240	AF528240 Hepatitis
c	54	20	100.0	150	14	AF528241	AF528241 Hepatitis
c	55	20	100.0	150	14	AF528242	AF528242 Hepatitis
c	56	20	100.0	150	14	AF528243	AF528243 Hepatitis
c	57	20	100.0	150	14	AF528244	AF528244 Hepatitis
c	58	20	100.0	150	14	AF528245	AF528245 Hepatitis
c	59	20	100.0	150	14	AF528246	AF528246 Hepatitis
c	60	20	100.0	150	14	AF528247	AF528247 Hepatitis
c	61	20	100.0	150	14	AF528248	AF528248 Hepatitis
c	62	20	100.0	150	14	AF528249	AF528249 Hepatitis
c	63	20	100.0	150	14	AF528250	AF528250 Hepatitis
c	64	20	100.0	150	14	AF528251	AF528251 Hepatitis
c	65	20	100.0	150	14	AF528252	AF528252 Hepatitis
c	66	20	100.0	150	14	AF528253	AF528253 Hepatitis
c	67	20	100.0	150	14	AF528254	AF528254 Hepatitis
c	68	20	100.0	150	14	AF528255	AF528255 Hepatitis
c	69	20	100.0	150	14	AF528256	AF528256 Hepatitis
c	70	20	100.0	150	14	AF528257	AF528257 Hepatitis
c	71	20	100.0	150	14	AF528258	AF528258 Hepatitis
c	72	20	100.0	150	14	AF528259	AF528259 Hepatitis
c	73	20	100.0	150	14	AF528261	AF528261 Hepatitis
c	74	20	100.0	150	14	AF528263	AF528263 Hepatitis
c	75	20	100.0	150	14	AF528264	AF528264 Hepatitis
c	76	20	100.0	150	14	AF528265	AF528265 Hepatitis
c	77	20	100.0	150	14	AF528266	AF528266 Hepatitis
c	78	20	100.0	150	14	AF528267	AF528267 Hepatitis
c	79	20	100.0	150	14	AF528268	AF528268 Hepatitis
c	80	20	100.0	150	14	AF528269	AF528269 Hepatitis
c	81	20	100.0	150	14	AF528270	AF528270 Hepatitis
c	82	20	100.0	150	14	AF528271	AF528271 Hepatitis
c	83	20	100.0	150	14	AF528272	AF528272 Hepatitis
c	84	20	100.0	150	14	AF528273	AF528273 Hepatitis
c	85	20	100.0	150	14	AF528274	AF528274 Hepatitis
c	86	20	100.0	150	14	AF528275	AF528275 Hepatitis
c	87	20	100.0	150	14	AF528276	AF528276 Hepatitis
c	88	20	100.0	150	14	AF528277	AF528277 Hepatitis
c	89	20	100.0	150	14	AF528278	AF528278 Hepatitis
c	90	20	100.0	150	14	AF528279	AF528279 Hepatitis
c	91	20	100.0	150	14	AF528280	AF528280 Hepatitis
c	92	20	100.0	150	14	AF528281	AF528281 Hepatitis

c 93	20	100.0	150	14	AF528282	AF528282 Hepatitis
c 94	20	100.0	150	14	AF528283	AF528283 Hepatitis
c 95	20	100.0	150	14	AF528284	AF528284 Hepatitis
c 96	20	100.0	150	14	AF528286	AF528286 Hepatitis
c 97	20	100.0	150	14	AF528287	AF528287 Hepatitis
c 98	20	100.0	150	14	AF528288	AF528288 Hepatitis
c 99	20	100.0	150	14	AF528289	AF528289 Hepatitis
c 100	20	100.0	150	14	AF528290	AF528290 Hepatitis

ALIGNMENTS

RESULT 1
AR027809
LOCUS AR027809 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5856459.
ACCESSION AR027809
VERSION AR027809.1 GI:5938629
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Frank,B.L., Roberts,P.C., Goodchild,J., Craig,J.Charles. and Mills,J.S.
TITLE Oligonucleotides specific for hepatitis B virus
JOURNAL Patent: US 5856459-A 7 05-JAN-1999;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
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Db 1 AGAGATGATTAGGCAGAGGT 20

RESULT 2
AX147024/c
LOCUS AX147024 27 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 18 from Patent WO0137291.
ACCESSION AX147024
VERSION AX147024.1 GI:14346295
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses thereof
JOURNAL Patent: WO 0137291-A 18 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
source 1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide primer (HBV reverse)"
modified_base 27
/note="derivatization with a p-(t-butyl)benzyl-residue"
/mod_base=OTHER
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
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Db 21 AGAGATGATTAGGCAGAGGT 2

RESULT 3
AR027810
LOCUS AR027810 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5856459.
ACCESSION AR027810
VERSION AR027810.1 GI:5938630
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Frank,B.L., Roberts,P.C., Goodchild,J., Craig,J.Charles. and Mills,J.S.
TITLE Oligonucleotides specific for hepatitis B virus
JOURNAL Patent: US 5856459-A 8 05-JAN-1999;
FEATURES Location/Qualifiers
source 1. .30
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
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Db 11 AGAGATGATTAGGCAGAGGT 30

RESULT 4
AR027840
LOCUS AR027840 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 38 from patent US 5856459.
ACCESSION AR027840
VERSION AR027840.1 GI:5938660
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Frank,B.L., Roberts,P.C., Goodchild,J., Craig,J.Charles. and Mills,J.S.
TITLE Oligonucleotides specific for hepatitis B virus
JOURNAL Patent: US 5856459-A 38 05-JAN-1999;
FEATURES Location/Qualifiers
source 1. .30
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
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Db 1 AGAGATGATTAGGCAGAGGT 20

RESULT 5
AX151115/c
LOCUS AX151115 87 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4 from Patent WO0138498.
ACCESSION AX151115
VERSION AX151115.1 GI:14533317
KEYWORDS .

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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stuyver,L., Schinazi,R., de Gendt,S., van Geyt,C., Zoulim,F.,
            Fried,M. and Rossau,R.
  TITLE     A new genotype of hepatitis b virus
  JOURNAL   Patent: WO 0138498-A 4 31-MAY-2001;
            Pharmasset, Inc. (US) ; INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .87
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 87;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 6
HPBPRECAA/c
LOCUS       HPBPRECAA                93 bp    DNA     linear   VRL 24-JAN-2003
DEFINITION  Hepatitis B virus variant B3 genomic RNA, entire pre-C region.
ACCESSION   D30625 D01192
VERSION     D30625.1  GI:484048
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Galibert,F., Mandart,E., Fitoussi,F., Tiollais,P. and Charnay,P.
  TITLE     Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
            cloned in E. coli
  JOURNAL   Nature 281 (5733), 646-650 (1979)
  MEDLINE   81012091
   PUBMED   399327
REFERENCE   2  (bases 1 to 93)
  AUTHORS   Li,J., Tong,S., Vitvitski,L., Zoulim,F. and Trepo,C.
  TITLE     Rapid detection and further characterization of infection with
            hepatitis B virus variants containing a stop codon in the distal
            pre-C region
  JOURNAL   J. Gen. Virol. 71 (Pt 9), 1993-1998 (1990)
  MEDLINE   91011344
   PUBMED   2212990
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
                     /note="HBeAg-negative HBV variant B3-pre-C region"
     gene            1. .93
                     /gene="pre-C/C"
     CDS             1. .>93
                     /gene="pre-C/C"
                     /codon_start=1
                     /product="pre-C/C protein"
                     /protein_id="BAA06312.1"
                     /db_xref="GI:507810"
                     /translation="MQLFHLCLIISCTCPTFQASKLCLGWLWGMD"
     variation       25
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="aa or ac"
     variation       37
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="t"
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                     E2"
                     /replace="t"
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                     E2"
                     /replace="g"
     variation       75
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                     /note="Base substitution has occurred at this position in
                     E2 and WO(wild-type)"
                     /replace="g"
     variation       87
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                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="cc"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 7
HPBPRECA/c
LOCUS       HPBPRECA                 99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type1 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76687
VERSION     M76687.1  GI:485341
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
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     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45507.1"
                     /db_xref="GI:485342"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
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     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 1 (creates internal stop
                     codon)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
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Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 8
HPBPRECB/c
LOCUS       HPBPRECB                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 2precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76688
VERSION     M76688.1  GI:485343
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     variation       2
                     /note="c in wt; t in virus type 2"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45508.1"
                     /db_xref="GI:485344"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 2 (creates internal stop
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ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 9
HPBPRECC/c
LOCUS       HPBPRECC                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 3precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76689
VERSION     M76689.1  GI:485345
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     variation       6
                     /note="c in wt; t in virus type 3"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45509.1"
                     /db_xref="GI:485346"
                     /translation="MQLFHLCLIISCSCPTFQASKLCLGWL"
     variation       58
                     /gene="C"
                     /note="g in wt; t in virus type 3 (val to phe)"
     variation       92
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                     /note="g in wt; a in virus type 3 (creates internal stop
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 10
HPBPRECD/c
LOCUS       HPBPRECD                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 4 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76690
VERSION     M76690.1  GI:485347
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45510.1"
                     /db_xref="GI:485348"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 4 (creates internal stop
                     codon)"
     variation       95
                     /note="g in wt; a in virus type 4 (gly to asp)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 11
HPBPRECE/c
LOCUS       HPBPRECE                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 5 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76691
VERSION     M76691.1  GI:485349
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45511.1"
                     /db_xref="GI:485350"
                     /translation="MQLFHLCLIISCSCPTVQPSKLCLGWL"
     variation       64. .67
                     /gene="C"
                     /note="gcc in wt; ccg in virus type 5 (ala to pro)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 5 (creates internal stop
                     codon)"
     variation       95
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 12
HPBPRECF/c
LOCUS       HPBPRECF                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 6 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76692
VERSION     M76692.1  GI:485351
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .99
                     /gene="C"
     misc_feature    10. .99
                     /gene="C"
                     /product="precore protein"
                     /note="putative cds"
     variation       11
                     /gene="C"
                     /note="t in wt; c in virus type 6 (loss of start codon)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 13
HPBPRECG/c
LOCUS       HPBPRECG                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 7 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76693
VERSION     M76693.1  GI:485352
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
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COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     misc_feature    10. .93
                     /gene="C"
                     /product="precore protein"
                     /standard_name="pre-C region note: putative CDS"
     variation       10
                     /gene="C"
                     /note="a in wt; t in virus type 7 (loss of start codon)"
     variation       14
                     /gene="C"
                     /note="a in wt; g in virus type 7 (gln to arg)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 7 ( creates internal stop
                     codon)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 14
HPBPRECH/c
LOCUS       HPBPRECH                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 8 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76694
VERSION     M76694.1  GI:485353
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     misc_feature    10. .93
                     /gene="C"
                     /product="precore protein"
                     /standard_name="pre-C region note: putative CDS"
     variation       12
                     /gene="C"
                     /note="g in wt; t in virus type 8 (loss of start codon)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 8 (creates internal stop
                     codon)"
     variation       95
                     /note="g in wt; a in virus type 8 (gly to asp)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 15
HPBPRECI/c
LOCUS       HPBPRECI                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 9 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76695
VERSION     M76695.1  GI:485354
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     misc_feature    10. .93
                     /gene="C"
                     /product="precore protein"
                     /standard_name="pre-C region note: putative CDS"
     variation       13
                     /gene="C"
                     /note="c in wt; t in virus type 9 (creates internal stop
                     codon)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 9 (creates internal stop
                     codon)"
     variation       95
                     /note="g in wt; a in virus type 9 (gly to asp)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 16
HPBPRECK/c
LOCUS       HPBPRECK                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 11 precore protein (pre-C region, C) gene,
            5' end.
ACCESSION   M76697
VERSION     M76697.1  GI:485357
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
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           Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE  1  (bases 1 to 99)
  AUTHORS  Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
           Will,H.
  TITLE    Prevalence and type of pre-C HBV mutants in anti-HBe positive
           carriers with chronic liver disease in a highly endemic area
  JOURNAL  Virology 183 (2), 840-844 (1991)
  MEDLINE  91306476
   PUBMED  1853582
COMMENT    Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .99
                     /gene="C"
     CDS             10. .>99
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45513.1"
                     /db_xref="GI:485358"
                     /translation="MQLFHLCLIISVHVLLFKPPSCALGGFGTW"
     variation       42. .43
                     /gene="C"
                     /note="frameshift mutation, deletion of single base in
                     virus type 11"
     variation       94
                     /gene="C"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity  100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 17
HPBPRECL/c
LOCUS      HPBPRECL                99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION Hepatitis B virus type 12 precore protein (pre-C region, C) gene,
           5' end.
ACCESSION  M76698
VERSION    M76698.1  GI:485359
KEYWORDS   e antigen; precore protein; tolerogen.
SOURCE     Hepatitis B virus
  ORGANISM Hepatitis B virus
           Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE  1  (bases 1 to 99)
  AUTHORS  Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
           Will,H.
  TITLE    Prevalence and type of pre-C HBV mutants in anti-HBe positive
           carriers with chronic liver disease in a highly endemic area
  JOURNAL  Virology 183 (2), 840-844 (1991)
  MEDLINE  91306476
   PUBMED  1853582
COMMENT    Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .99
                     /gene="C"
     CDS             10. .>99
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45514.1"
                     /db_xref="GI:485360"
                     /translation="MQLFHLCLIISVHVLLFKPPSCALGGFRTW"
     variation       41. .42
                     /gene="C"
                     /note="frameshift mutation, deletion of single base in
                     virus type 12"
     variation       90
                     /gene="C"
                     /note="t in wt position 91; a in virus type 12 position
                     90"
     variation       93
                     /gene="C"
                     /note="g in wt position 94; a in virus type 12 position
                     93"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity  100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 18
HPBPRECM/c
LOCUS      HPBPRECM                99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION Hepatitis B virus type 13 precore protein (pre-C region, C) gene,
           5' end.
ACCESSION  M76699
VERSION    M76699.1  GI:485361
KEYWORDS   e antigen; precore protein; tolerogen.
SOURCE     Hepatitis B virus
  ORGANISM Hepatitis B virus
           Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE  1  (bases 1 to 99)
  AUTHORS  Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
           Will,H.
  TITLE    Prevalence and type of pre-C HBV mutants in anti-HBe positive
           carriers with chronic liver disease in a highly endemic area
  JOURNAL  Virology 183 (2), 840-844 (1991)
  MEDLINE  91306476
   PUBMED  1853582
COMMENT    Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .99
                     /gene="C"
     CDS             10. .>99
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45515.1"
                     /db_xref="GI:485362"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWDM"
     variation       95
                     /gene="C"
                     /note="g in wt; a in virus type 13 (gly to asp)"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity  100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
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Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 19
AX151114/c
LOCUS       AX151114                 129 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3 from Patent WO0138498.
ACCESSION   AX151114
VERSION     AX151114.1  GI:14533316
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stuyver,L., Schinazi,R., de Gendt,S., van Geyt,C., Zoulim,F.,
            Fried,M. and Rossau,R.
  TITLE     A new genotype of hepatitis b virus
  JOURNAL   Patent: WO 0138498-A 3 31-MAY-2001;
            Pharmasset, Inc. (US) ; INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .129
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 129;
  Best Local Similarity  100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 20
AF528205/c
LOCUS       AF528205                 150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1123 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528205
VERSION     AF528205.1  GI:32810971
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1123"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87556.1"
                     /db_xref="GI:32810972"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLXG"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 21
AF528206/c
LOCUS       AF528206                 150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1112 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528206
VERSION     AF528206.1  GI:32810973
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1112"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87557.1"
                     /db_xref="GI:32810974"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLXG"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 22
AF528207/c
LOCUS       AF528207                 150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC20 core antigen precursor, gene, partial cds.
ACCESSION   AF528207
VERSION     AF528207.1  GI:32810975
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
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            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC20"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87558.1"
                     /db_xref="GI:32810976"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 23
AF528208/c
LOCUS       AF528208                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC340 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528208
VERSION     AF528208.1  GI:32810977
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC340"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 24
AF528209/c
LOCUS       AF528209                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC58 core antigen precursor, gene, partial cds.
ACCESSION   AF528209
VERSION     AF528209.1  GI:32810978
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC58"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87559.1"
                     /db_xref="GI:32810979"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 25
AF528210/c
LOCUS       AF528210                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC470 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528210
VERSION     AF528210.1  GI:32810980
KEYWORDS    .
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SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC470"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
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Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 26
AF528211/c
LOCUS       AF528211                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC335 core antigen precursor, gene, partial cds.
ACCESSION   AF528211
VERSION     AF528211.1  GI:32810981
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC335"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87560.1"
                     /db_xref="GI:32810982"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
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Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 27
AF528212/c
LOCUS       AF528212                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC343 core antigen precursor, gene, partial cds.
ACCESSION   AF528212
VERSION     AF528212.1  GI:32810983
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC343"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87561.1"
                     /db_xref="GI:32810984"
                     /translation="MQLFHLCLIISCSCPTIQASKLCLGWLWG"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 28
AF528213/c
LOCUS       AF528213                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC404 core antigen precursor, gene, partial cds.
ACCESSION   AF528213
VERSION     AF528213.1  GI:32810985
KEYWORDS    .
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SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC404"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87562.1"
                     /db_xref="GI:32810986"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 29
AF528214/c
LOCUS       AF528214                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC423 core antigen precursor, gene, partial cds.
ACCESSION   AF528214
VERSION     AF528214.1  GI:32810987
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC423"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87563.1"
                     /db_xref="GI:32810988"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWD"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 30
AF528215/c
LOCUS       AF528215                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC424 core antigen precursor, gene, partial cds.
ACCESSION   AF528215
VERSION     AF528215.1  GI:32810989
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC424"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87564.1"
                     /db_xref="GI:32810990"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 31
AF528216/c
LOCUS       AF528216                150 bp    DNA     linear   VRL 31-JUL-2003
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DEFINITION  Hepatitis B virus ASC1035 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528216
VERSION     AF528216.1  GI:32810991
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1035"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87565.1"
                     /db_xref="GI:32810992"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 32
AF528217/c
LOCUS       AF528217                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1061 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528217
VERSION     AF528217.1  GI:32810993
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1061"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 33
AF528218/c
LOCUS       AF528218                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC339 core antigen precursor, gene, partial cds.
ACCESSION   AF528218
VERSION     AF528218.1  GI:32810994
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC339"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87566.1"
                     /db_xref="GI:32810995"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 34
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AF528219/c
LOCUS       AF528219                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC295 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528219
VERSION     AF528219.1  GI:32810996
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC295"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
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Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 35
AF528220/c
LOCUS       AF528220                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1027 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528220
VERSION     AF528220.1  GI:32810997
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1027"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 36
AF528221/c
LOCUS       AF528221                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1029 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528221
VERSION     AF528221.1  GI:32810998
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1029"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 37
AF528222/c
LOCUS       AF528222                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC298 core antigen precursor, gene, partial cds.
ACCESSION   AF528222
VERSION     AF528222.1  GI:32810999
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KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC298"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87567.1"
                     /db_xref="GI:32811000"
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ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 38
AF528224/c
LOCUS       AF528224                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC263 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528224
VERSION     AF528224.1  GI:32811002
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC263"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 39
AF528225/c
LOCUS       AF528225                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1036 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528225
VERSION     AF528225.1  GI:32811003
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1036"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 40
AF528226/c
LOCUS       AF528226                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1062 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528226
VERSION     AF528226.1  GI:32811004
KEYWORDS    .
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SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1062"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 41
AF528227/c
LOCUS       AF528227                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1065 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528227
VERSION     AF528227.1  GI:32811005
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1065"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 42
AF528228/c
LOCUS       AF528228                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1072 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528228
VERSION     AF528228.1  GI:32811006
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1072"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 43
AF528229/c
LOCUS       AF528229                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1074 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528229
VERSION     AF528229.1  GI:32811007
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
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  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1074"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 44
AF528231/c
LOCUS       AF528231                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1091 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528231
VERSION     AF528231.1  GI:32811009
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis B virus"
                     /proviral
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                     /isolate="ASC1091"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 45
AF528232/c
LOCUS       AF528232                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC265 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528232
VERSION     AF528232.1  GI:32811010
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC265"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 46
AF528233/c
LOCUS       AF528233                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC262 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528233
VERSION     AF528233.1  GI:32811011
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
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  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC262"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 47
AF528234/c
LOCUS       AF528234                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1109 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528234
VERSION     AF528234.1  GI:32811012
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
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                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 48
AF528235/c
LOCUS       AF528235                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1275 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528235
VERSION     AF528235.1  GI:32811013
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
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                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
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                     /product="core antigen precursor"
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ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 49
AF528236/c
LOCUS       AF528236                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1274 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528236
VERSION     AF528236.1  GI:32811015
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
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  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
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                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
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                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 50
AF528237/c
LOCUS       AF528237                 150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1090 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528237
VERSION     AF528237.1  GI:32811016
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1090"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
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                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 15, 2004, 09:10:16 ; Search time 181 Seconds
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Title: US-08-901-612A-7
Perfect score: 20
Sequence: 1 agagatgattaggcagaggt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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9: geneseqn2003bs:*
10: geneseqn2003cs:*
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12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	2	AAT72560	Aat72560 Hepatitis
	2	20	100.0	20	2	AAT72561	Aat72561 Hepatitis
	3	20	100.0	25	3	AAA88131	Aaa88131 SP6 RNA p
c	4	20	100.0	27	4	AAH25416	Aah25416 Reverse P
	5	20	100.0	30	2	AAT72562	Aat72562 Hepatitis
	6	20	100.0	30	2	AAT72614	Aat72614 Hepatitis
	7	20	100.0	30	2	AAT72563	Aat72563 Hepatitis
	8	20	100.0	30	2	AAT72615	Aat72615 Hepatitis
c	9	20	100.0	39	10	ADC64742	Adc64742 Hepatitis
c	10	20	100.0	64	3	AAA88130	Aaa88130 SP6 RNA p
c	11	20	100.0	87	4	AAD09094	Aad09094 Hepatitis
c	12	20	100.0	129	4	AAD09093	Aad09093 Hepatitis
c	13	20	100.0	250	6	ABK29867	Abk29867 Wild type
c	14	20	100.0	639	6	AAD27422	Aad27422 Hepatitis
c	15	20	100.0	639	6	AAD31509	Aad31509 Hepatitis
c	16	20	100.0	646	12	ADL56756	Adl56756 HBV preco
c	17	20	100.0	655	2	AAQ47014	Aaq47014 HBV (adw)
c	18	20	100.0	655	2	AAT35649	Aat35649 Precore/c
c	19	20	100.0	655	4	AAH77569	Aah77569 HBV genot
c	20	20	100.0	655	4	AAH77568	Aah77568 HBV genot
c	21	20	100.0	655	4	AAH77574	Aah77574 HBV genot
c	22	20	100.0	655	4	AAH77573	Aah77573 HBV genot
c	23	20	100.0	655	4	AAH77570	Aah77570 HBV genot
c	24	20	100.0	655	4	AAH77571	Aah77571 HBV genot
c	25	20	100.0	655	4	AAD21244	Aad21244 Hepatitis
c	26	20	100.0	655	9	ABX80077	Abx80077 Hepatitis
c	27	20	100.0	655	10	ABX96938	Abx96938 Hepatitis
c	28	20	100.0	660	1	AAN91081	Aan91081 DNA seque
c	29	20	100.0	664	4	AAH77572	Aah77572 HBV genot
c	30	20	100.0	669	12	ADO07220	Ado07220 Hepatitis
c	31	20	100.0	673	4	AAD09092	Aad09092 Hepatitis
c	32	20	100.0	675	4	AAH77563	Aah77563 HBV preCo
c	33	20	100.0	681	4	AAH77566	Aah77566 HBV genot
c	34	20	100.0	681	4	AAH77567	Aah77567 HBV genot
c	35	20	100.0	750	1	AAN80943	Aan80943 HBV core
c	36	20	100.0	909	6	AAH77169	Aah77169 Regulator
c	37	20	100.0	1334	2	AAV82691	Aav82691 Fulminant
c	38	20	100.0	1395	2	AAV82688	Aav82688 Fulminant
c	39	20	100.0	1400	2	AAV82687	Aav82687 Fulminant
c	40	20	100.0	1445	2	AAV82692	Aav82692 Fulminant
c	41	20	100.0	1445	2	AAV82685	Aav82685 Fulminant
c	42	20	100.0	1445	2	AAV82690	Aav82690 Fulminant
c	43	20	100.0	1445	2	AAV82684	Aav82684 Fulminant
c	44	20	100.0	1500	2	AAV82695	Aav82695 Fulminant
c	45	20	100.0	1500	2	AAV82683	Aav82683 Fulminant
c	46	20	100.0	1500	2	AAV82694	Aav82694 Fulminant
c	47	20	100.0	1500	2	AAV82686	Aav82686 Fulminant
c	48	20	100.0	1500	2	AAV82706	Aav82706 Wild type
c	49	20	100.0	1500	2	AAV82689	Aav82689 Fulminant
c	50	20	100.0	1500	2	AAV82693	Aav82693 Fulminant
c	51	20	100.0	1977	12	ADJ53703	Adj53703 RNA pseud
c	52	20	100.0	2342	1	AAN93072	Aan93072 Sequence
c	53	20	100.0	2743	1	AAN00003	Aan00003 Sequence
c	54	20	100.0	2743	2	AAQ04799	Aaq04799 Recombina
c	55	20	100.0	3180	4	AAH42375	Aah42375 Nucleotid
c	56	20	100.0	3182	6	AAD31765	Aad31765 Hepatitis
c	57	20	100.0	3182	9	ACA62422	Aca62422 Hepatitis
c	58	20	100.0	3182	10	AAD60866	Aad60866 Hepatitis
c	59	20	100.0	3183	1	AAN30035	Aan30035 DNA contg
c	60	20	100.0	3200	1	AAN40243	Aan40243 DNA encod
c	61	20	100.0	3200	1	AAN70165	Aan70165 Entire nu
c	62	20	100.0	3220	3	AAZ88924	Aaz88924 Hepatitis
c	63	20	100.0	3221	2	AAZ23281	Aaz23281 DNA seque
c	64	20	100.0	3221	4	AAH42374	Aah42374 Nucleotid
c	65	20	100.0	3221	6	ABK23902	Abk23902 Bee venom
c	66	20	100.0	3221	6	ABS70986	Abs70986 DNA encod
c	67	20	100.0	3221	6	ABS66412	Abs66412 Hepatitis
c	68	20	100.0	3221	10	ADD27773	Add27773 HBV subty
c	69	20	100.0	3248	4	AAD09091	Aad09091 Hepatitis
c	70	20	100.0	3248	4	AAH77562	Aah77562 HBV genot
c	71	20	100.0	4084	4	AAD14316	Aad14316 Hepatitis
c	72	20	100.0	4496	4	AAD14317	Aad14317 Hepatitis
c	73	20	100.0	5618	2	AAQ88310	Aaq88310 Plasmid p
c	74	20	100.0	5639	2	AAX57972	Aax57972 Recombina
c	75	20	100.0	6371	2	AAZ23292	Aaz23292 DNA seque
c	76	20	100.0	6371	2	AAZ23285	Aaz23285 DNA seque
c	77	20	100.0	6375	2	AAZ23294	Aaz23294 DNA seque
c	78	20	100.0	7991	6	AAS16094	Aas16094 HBV viral
c	79	20	100.0	8007	6	AAS16092	Aas16092 HBV viral
c	80	20	100.0	8717	6	AAS16093	Aas16093 HBV viral
c	81	20	100.0	9325	2	AAZ23282	Aaz23282 DNA seque
	82	20	100.0	9534	2	AAT62072	Aat62072 Vector RP
c	83	20	100.0	9859	2	AAZ23286	Aaz23286 DNA seque
c	84	19.6	98.0	33	12	ADM16809	Adm16809 Hepatitis
c	85	19.2	96.0	30	2	AAQ45797	Aaq45797 HBV ampli
c	86	19.2	96.0	30	2	AAV07794	Aav07794 HBV.D44 a
c	87	19.2	96.0	30	2	AAV83023	Aav83023 Amplifier
	88	19.2	96.0	50	2	AAQ06722	Aaq06722 :HBV.LLA2
c	89	19	95.0	19	11	ADL99951	Adl99951 Hepatitis
	90	19	95.0	19	11	ADM00598	Adm00598 Hepatitis
c	91	19	95.0	20	2	AAQ37777	Aaq37777 Probe PR1
c	92	19	95.0	20	5	AAC88880	Aac88880 HBV polyA
c	93	19	95.0	20	6	ABT08252	Abt08252 Human ade
c	94	19	95.0	20	12	ADF09463	Adf09463 E1-delete

c	95	19	95.0	22	2	AAT73885	Aat73885 Human hep
c	96	19	95.0	87	2	AAT05545	Aat05545 Human hep
c	97	19	95.0	94	2	AAT73892	Aat73892 Human hep
c	98	19	95.0	94	2	AAT73890	Aat73890 Human hep
c	99	19	95.0	94	2	AAT73887	Aat73887 Human hep
c	100	19	95.0	94	2	AAT73889	Aat73889 Human hep

ALIGNMENTS

RESULT 1
AAT72560
ID AAT72560 standard; DNA; 20 BP.
XX
AC AAT72560;
XX
DT 03-SEP-1997 (first entry)
XX
DE Hepatitis B virus RNA antisense oligonucleotide HBV43a.
XX
KW HBV; HBV infection; inhibition; replication; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .20
FT /*tag= a
FT /note= "Internucleotide linkages are phosphorothioate"
XX
PN WO9639502-A1.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002432.
XX
PR 06-JUN-1995; 95US-00467397.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
PI Craig CJ, Frank BL, Goodchild J, Jupp R, Kilkuskie RE, Mills JS;
PI Roberts NA, Roberts PC, Slade A;
XX
DR WPI; 1997-043124/04.
XX
PT Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT used in the detection and treatment of HBV infection.
XX
PS Claim 1; Page 12; 81pp; English.
XX
CC The present sequence represents a synthetic oligonucleotide HBV43a which
CC is complementary to a portion of the hepatitis B virus (HBV) RNA. The
CC antisense oligonucleotide may be used to detect the presence of HBV in a
CC sample. The antisense oligonucleotide, and oligonucleotides containing a
CC sequence which is complementary to at least two non- contiguous regions
CC of an HBV nucleic acid, may be used for inhibiting HBV replication in a
CC cell or for the treatment of HBV infection
XX
SQ Sequence 20 BP; 7 A; 1 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGAGATGATTAGGCAGAGGT 20
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Db          1 AGAGATGATTAGGCAGAGGT 20
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RESULT 2
AAT72561
ID AAT72561 standard; DNA; 20 BP.
XX
AC AAT72561;
XX
DT 03-SEP-1997 (first entry)
XX
DE Hepatitis B virus RNA antisense oligonucleotide HBV43Ma.
XX
KW HBV; HBV infection; inhibition; replication; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /note= "Internucleotide linkages are phosphorothioate"
FT misc_RNA 1. .10
FT /*tag= b
FT /note= "2'-OMe RNA"
FT modified_base 1
FT /*tag= c
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FT /note= "2'-O-methyladenosine"
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FT /*tag= d
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FT /*tag= e
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FT /mod_base= gm
FT modified_base 5
FT /*tag= g
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FT /*tag= h
FT /mod_base= um
FT modified_base 7
FT /*tag= i
FT /mod_base= gm
FT modified_base 8
FT /*tag= j
FT /mod_base= OTHER
FT /note= "2'-O-methyladenosine"
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FT /*tag= k
FT /mod_base= um
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XX
PN WO9639502-A1.
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PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002432.
XX
PR 06-JUN-1995; 95US-00467397.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
PI Craig CJ, Frank BL, Goodchild J, Jupp R, Kilkuskie RE, Mills JS;
PI Roberts NA, Roberts PC, Slade A;
XX
DR WPI; 1997-043124/04.
XX
PT Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT used in the detection and treatment of HBV infection.
XX
PS Claim 1; Page 12; 81pp; English.

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XX
CC   The present sequence represents a synthetic oligonucleotide HBV43Ma which
CC   is complementary to a portion of the hepatitis B virus (HBV) RNA. The
CC   antisense oligonucleotide may be used to detect the presence of HBV in a
CC   sample. The antisense oligonucleotide, and oligonucleotides containing a
CC   sequence which is complementary to at least two non- contiguous regions
CC   of an HBV nucleic acid, may be used for inhibiting HBV replication in a
CC   cell or for the treatment of HBV infection
XX
SQ   Sequence 20 BP; 7 A; 1 C; 8 G; 1 T; 3 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 5.8;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||:||::||||||||||
Db          1 AGAGAUGAUUAGGCAGAGGT 20


RESULT 3
AAA88131
ID   AAA88131 standard; RNA; 25 BP.
XX
AC   AAA88131;
XX
DT   15-SEP-2003  (revised)
DT   13-DEC-2000  (first entry)
XX
DE   SP6 RNA polymerase promoter sequence SEQ ID NO:3.
XX
KW   Hepatitis B virus; HBV; detection; probe; promoter; ss.
XX
OS   Enterobacteria phage SP6.
XX
PN   US6100024-A.
XX
PD   08-AUG-2000.
XX
PF   08-FEB-1991;   91US-00652888.
XX
PR   08-FEB-1991;   91US-00652888.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Hudson GR,  Dimond RL,  Schumm JW;
XX
DR   WPI; 2000-542420/49.
XX
PT   Single-stranded DNA probe comprising an anti-target nucleic acid, a (-)-
PT   promoter segment linked to the anti-target segment and a reporter
PT   segment, useful for detecting a target nucleic acid, e.g. hepatitis B
PT   virus, in a sample.
XX
PS   Example 3; Col 19-20; 18pp; English.
XX
CC   The present invention describes a single-stranded DNA probe (I)
CC   comprising in 3'-5' order, an anti-target nucleic acid segment, a (-)-
CC   promoter segment functionally linked to the anti-target segment, and a
CC   nucleic acid reporter segment. The probe is useful for testing a sample
CC   of a nucleic acid for the presence of a target nucleic acid segment or
CC   for detecting a target nucleic acid segment in a sample. The probe may
CC   also be used for the detection of hepatitis B virus (HBV). The present
CC   sequence represents a bacteriophage SP6 RNA polymerase promoter sequence
CC   which is used in an example from the present invention. (Updated on 15-
CC   SEP-2003 to standardise OS field)
XX
SQ   Sequence 25 BP; 10 A; 1 C; 10 G; 0 T; 4 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 3;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 5.9;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||:||::|||||||||:
Db          3 AGAGAUGAUUAGGCAGAGGU 22


RESULT 4
AAH25416/c
ID   AAH25416 standard; DNA; 27 BP.
XX
AC   AAH25416;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Reverse PCR primer used to amplify a HBV DNA fragment.
XX
KW   Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   27
FT                   /*tag=  a
FT                   /note= "derivatisation with a p-(t-butyl)benzyl-residue"
XX
PN   WO200137291-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP011459.
XX
PR   17-NOV-1999;   99EP-00122853.
PR   12-MAY-2000; 2000EP-00110165.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Weindel K,  Riedling M,  Geiger A;
XX
DR   WPI; 2001-381247/40.
XX
PT   Novel composition of magnetic glass particles for purification of DNA or
PT   RNA in automated processes.
XX
PS   Example 7; Page 99; 105pp; English.
XX
CC   The specification describes a composition of magnetic glass particles,
CC   which contain at least one magnetic object with a mean diameter between 5
CC   -500 nm. The composition is useful for the purification of nucleic acids.
CC   The composition can be used to process large quantities of nucleic acid
CC   samples, because it does not involve the particles being centrifuged or
CC   the fluids being drawn through glass fiber filters. PCR primers AAH25415-
CC   16 were used to amplify HBV DNA fragments. The amplified fragment can be
CC   purified using the method of the invention
XX
SQ   Sequence 27 BP; 5 A; 10 C; 2 G; 10 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         21 AGAGATGATTAGGCAGAGGT 2


RESULT 5
AAT72562
ID   AAT72562 standard; DNA; 30 BP.
XX
AC   AAT72562;
XX
DT   03-SEP-1997  (first entry)
XX
DE   Hepatitis B virus RNA antisense oligonucleotide HBV88b.
```

```
XX
KW   HBV; HBV infection; inhibition; replication; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .30
FT                   /*tag=  a
FT                   /note= "Internucleotide linkages are phosphorothioate"
XX
PN   WO9639502-A1.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002432.
XX
PR   06-JUN-1995;   95US-00467397.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Craig CJ,  Frank BL,  Goodchild J,  Jupp R,  Kilkuskie RE,  Mills JS;
PI   Roberts NA,  Roberts PC,  Slade A;
XX
DR   WPI; 1997-043124/04.
XX
PT   Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT   used in the detection and treatment of HBV infection.
XX
PS   Claim 1; Page 12; 81pp; English.
XX
CC   The present sequence represents a synthetic oligonucleotide HBV88b which
CC   is complementary to a portion of the hepatitis B virus (HBV) RNA. The
CC   antisense oligonucleotide may be used to detect the presence of HBV in a
CC   sample. The antisense oligonucleotide, and oligonucleotides containing a
CC   sequence which is complementary to at least two non- contiguous regions
CC   of an HBV nucleic acid, may be used for inhibiting HBV replication in a
CC   cell or for the treatment of HBV infection
XX
SQ   Sequence 30 BP; 12 A; 3 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         11 AGAGATGATTAGGCAGAGGT 30


RESULT 6
AAT72614
ID   AAT72614 standard; DNA; 30 BP.
XX
AC   AAT72614;
XX
DT   04-SEP-1997  (first entry)
XX
DE   Hepatitis B virus RNA antisense oligonucleotide HBV-87b.
XX
KW   HBV; HBV infection; inhibition; replication; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .30
FT                   /*tag=  a
FT                   /note= "Internucleotide linkages are phosphorothioate"
XX
PN   WO9639502-A1.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002432.
XX
PR   06-JUN-1995;   95US-00467397.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Craig CJ,  Frank BL,  Goodchild J,  Jupp R,  Kilkuskie RE,  Mills JS;
PI   Roberts NA,  Roberts PC,  Slade A;
XX
DR   WPI; 1997-043124/04.
XX
PT   Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT   used in the detection and treatment of HBV infection.
XX
PS   Claim 5; Page 15; 81pp; English.
XX
CC   The present sequence represents a synthetic oligonucleotide HBV-87b which
CC   contains a sequence which is complementary to at least two non-contiguous
CC   regions of a hepatitis B virus (HBV) nucleic acid. The antisense
CC   oligonucleotide may be used to detect the presence of HBV in a sample.
CC   The antisense oligonucleotide, and oligonucleotides complementary to a
CC   portion of the HBV RNA, may be used for inhibiting HBV replication in a
CC   cell or for the treatment of HBV infection
XX
SQ   Sequence 30 BP; 10 A; 2 C; 12 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db          1 AGAGATGATTAGGCAGAGGT 20


RESULT 7
AAT72563
ID   AAT72563 standard; DNA; 30 BP.
XX
AC   AAT72563;
XX
DT   03-SEP-1997  (first entry)
XX
DE   Hepatitis B virus RNA antisense oligonucleotide HBV88Mb.
XX
KW   HBV; HBV infection; inhibition; replication; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .30
FT                   /*tag=  a
FT                   /note= "Internucleotide linkages are phosphorothioate"
FT   misc_RNA        1. .20
FT                   /*tag=  b
FT                   /note= "2'-OMe RNA"
FT   modified_base   1
FT                   /*tag=  c
FT                   /mod_base= gm
FT   modified_base   2
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   3
FT                   /*tag=  e
FT                   /mod_base= cm
FT   modified_base   4
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   5
FT                   /*tag=  g
```

```
FT                   /mod_base= um
FT   modified_base   6
FT                   /*tag=  h
FT                   /mod_base= gm
FT   modified_base   7
FT                   /*tag=  i
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   8
FT                   /*tag=  j
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   9
FT                   /*tag=  k
FT                   /mod_base= cm
FT   modified_base   10
FT                   /*tag=  l
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   11
FT                   /*tag=  m
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   12
FT                   /*tag=  n
FT                   /mod_base= gm
FT   modified_base   13
FT                   /*tag=  o
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   14
FT                   /*tag=  p
FT                   /mod_base= gm
FT   modified_base   15
FT                   /*tag=  q
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   16
FT                   /*tag=  r
FT                   /mod_base= um
FT   modified_base   17
FT                   /*tag=  s
FT                   /mod_base= gm
FT   modified_base   18
FT                   /*tag=  s
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   19
FT                   /*tag=  u
FT                   /mod_base= um
FT   modified_base   20
FT                   /*tag=  v
FT                   /mod_base= um
XX
PN   WO9639502-A1.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002432.
XX
PR   06-JUN-1995;   95US-00467397.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Craig CJ,  Frank BL,  Goodchild J,  Jupp R,  Kilkuskie RE,  Mills JS;
PI   Roberts NA,  Roberts PC,  Slade A;
XX
DR   WPI; 1997-043124/04.
XX
PT   Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT   used in the detection and treatment of HBV infection.
XX
PS   Claim 1; Page 12; 81pp; English.
XX
CC   The present sequence represents a synthetic oligonucleotide HBV88Mb which
CC   is complementary to a portion of the hepatitis B virus (HBV) RNA. The
CC   antisense oligonucleotide may be used to detect the presence of HBV in a
CC   sample. The antisense oligonucleotide, and oligonucleotides containing a
CC   sequence which is complementary to at least two non- contiguous regions
CC   of an HBV nucleic acid, may be used for inhibiting HBV replication in a
CC   cell or for the treatment of HBV infection
XX
SQ   Sequence 30 BP; 12 A; 3 C; 10 G; 1 T; 4 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   85.0%;  Pred. No. 6;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||:||::||||||||||
Db         11 AGAGAUGAUUAGGCAGAGGT 30


RESULT 8
AAT72615
ID   AAT72615 standard; DNA; 30 BP.
XX
AC   AAT72615;
XX
DT   04-SEP-1997  (first entry)
XX
DE   Hepatitis B virus RNA antisense oligonucleotide HBV-87Mb.
XX
KW   HBV; HBV infection; inhibition; replication; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .30
FT                   /*tag=  a
FT                   /note= "Internucleotide linkages are phosphorothioate"
FT   misc_RNA        1. .10
FT                   /*tag=  b
FT                   /note= "2'-OMe RNA"
FT   modified_base   1
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   2
FT                   /*tag=  d
FT                   /mod_base= gm
FT   modified_base   3
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   4
FT                   /*tag=  f
FT                   /mod_base= gm
FT   modified_base   5
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   6
FT                   /*tag=  h
FT                   /mod_base= um
FT   modified_base   7
FT                   /*tag=  i
FT                   /mod_base= gm
FT   modified_base   8
FT                   /*tag=  j
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   9
FT                   /*tag=  k
FT                   /mod_base= um
```

```
FT   modified_base   10
FT                   /*tag=  1
FT                   /mod_base= um
XX
PN   WO9639502-A1.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002432.
XX
PR   06-JUN-1995;   95US-00467397.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Craig CJ,  Frank BL,  Goodchild J,  Jupp R,  Kilkuskie RE,  Mills JS;
PI   Roberts NA,  Roberts PC,  Slade A;
XX
DR   WPI; 1997-043124/04.
XX
PT   Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT   used in the detection and treatment of HBV infection.
XX
PS   Claim 5; Page 15; 81pp; English.
XX
CC   The present sequence represents a synthetic oligonucleotide HBV-87Mb
CC   which contains a sequence which is complementary to at least two non-
CC   contiguous regions of a hepatitis B virus (HBV) nucleic acid. The
CC   antisense oligonucleotide may be used to detect the presence of HBV in a
CC   sample. The antisense oligonucleotide, and oligonucleotides complementary
CC   to a portion of the HBV RNA, may be used for inhibiting HBV replication
CC   in a cell or for the treatment of HBV infection
XX
SQ   Sequence 30 BP; 10 A; 2 C; 12 G; 3 T; 3 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   85.0%;  Pred. No. 6;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||:||::||||||||||
Db          1 AGAGAUGAUUAGGCAGAGGT 20


RESULT 9
ADC64742/c
ID   ADC64742 standard; RNA; 39 BP.
XX
AC   ADC64742;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Hepatitis B virus DNA polymerase related RNA oligonucleotide.
XX
KW   screening; antiviral; hepatitis B virus; HBV; DNA polymerase; ss.
XX
OS   Synthetic.
OS   Hepatitis B virus.
XX
PN   KR2002007891-A.
XX
PD   29-JAN-2002.
XX
PF   19-JUL-2000; 2000KR-00041420.
XX
PR   19-JUL-2000; 2000KR-00041420.
XX
PA   (MOGA-) MOGAM BIOTECHNOLOGY INST.
PA   (VIRO-) VIROGEN CO LTD.
XX
PI   Ji HJ,  Jung SI,  Kim YC,  Min MG,  Ryu WS,  Yoon GS;
XX
DR   WPI; 2003-309015/30.
XX
PT   Screening of antiviral agents by protein-priming activity of hepatitis B
PT   virus DNA polymerase.
XX
PS   Disclosure; Page 12; 13pp; Korean.
XX
CC   The present invention describes a method of screening for an antiviral
CC   agent by the protein-priming activity of hepatitis B virus (HBV) DNA
CC   polymerase. Also described is developing an antiviral agent with a high
CC   selectivity to HBV which can be used for high-throughput screening. The
CC   present sequence represents an RNA oligonucleotide which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 39 BP; 5 A; 13 C; 3 G; 0 T; 18 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 10;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         27 AGAGATGATTAGGCAGAGGT 8


RESULT 10
AAA88130/c
ID   AAA88130 standard; DNA; 64 BP.
XX
AC   AAA88130;
XX
DT   15-SEP-2003  (revised)
DT   13-DEC-2000  (first entry)
XX
DE   SP6 RNA polymerase promoter sequence SEQ ID NO:2.
XX
KW   Hepatitis B virus; HBV; detection; probe; promoter; ds.
XX
OS   Enterobacteria phage SP6.
XX
PN   US6100024-A.
XX
PD   08-AUG-2000.
XX
PF   08-FEB-1991;   91US-00652888.
XX
PR   08-FEB-1991;   91US-00652888.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Hudson GR,  Dimond RL,  Schumm JW;
XX
DR   WPI; 2000-542420/49.
XX
PT   Single-stranded DNA probe comprising an anti-target nucleic acid, a (-)-
PT   promoter segment linked to the anti-target segment and a reporter
PT   segment, useful for detecting a target nucleic acid, e.g. hepatitis B
PT   virus, in a sample.
XX
PS   Example 3; Col 19-20; 18pp; English.
XX
CC   The present invention describes a single-stranded DNA probe (I)
CC   comprising in 3'-5' order, an anti-target nucleic acid segment, a (-)-
CC   promoter segment functionally linked to the anti-target segment, and a
CC   nucleic acid reporter segment. The probe is useful for testing a sample
CC   of a nucleic acid for the presence of a target nucleic acid segment or
CC   for detecting a target nucleic acid segment in a sample. The probe may
CC   also be used for the detection of hepatitis B virus (HBV). The present
CC   sequence represents a bacteriophage SP6 RNA polymerase promoter sequence
CC   which is used in an example from the present invention. (Updated on 15-
CC   SEP-2003 to standardise OS field)
XX
SQ   Sequence 64 BP; 14 A; 22 C; 4 G; 24 T; 0 U; 0 Other;
```

```
  Query Match           100.0%;  Score 20;  DB 3;  Length 64;
  Best Local Similarity  100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         23 AGAGATGATTAGGCAGAGGT 4


RESULT 11
AAD09094/c
ID   AAD09094 standard; DNA; 87 BP.
XX
AC   AAD09094;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Hepatitis B virus FR1 strain genotype G HBeAg DNA fragment.
XX
KW   HBV genotype G; precore; HBpol; polymerase; envelope protein; preS1;
KW   preS2; surface antigen; HBsAg; HBX protein; vaccine; HBeAg;
KW   liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200138498-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US032108.
XX
PR   24-NOV-1999;   99US-0167206P.
XX
PA   (PHAR-) PHARMASSET INC.
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Schinazi R,  De Gendt S,  Van Geyt C,  Zoulim F,  Fried M;
PI   Rossau R;
XX
DR   WPI; 2001-367676/38.
XX
PT   Novel hepatitis B virus genotype G, nucleic acids encoding virus,
PT   polypeptides encoded by nucleic acids, useful for preparing vaccine to
PT   treat or prevent the hepatitis B virus genotype G infection in a subject.
XX
PS   Claim 6; Page 57; 84pp; English.
XX
CC   The present invention relates to hepatitis B virus (HBV) strain FR1,
CC   genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1,
CC   PreS2 and surface antigen HBsAg) and HBX proteins. HBV genotype G nucleic
CC   acids and polypeptides are useful for diagnosing, prognosing and treating
CC   infections caused by HBV genotype G. They can be used in a vaccine to
CC   treat or prevent HBV genotype G infection. The HBV genotype G derived
CC   nucleic acids and antibodies are useful for detecting HBV genotype G in a
CC   sample or diagnosis of HBV genotype G infection. The presence of HBV
CC   genotype G statistically correlates with the presence of liver damage
CC   and/or liver cancer in the subject. The HBV genotype G core insert
CC   peptide encoding nucleic acid is useful for designing monitoring assays
CC   to study and predict the evolution of anti-HBe and anti-HBc antibodies
CC   and HBeAg (genotype G e antigen) in patients infected with HBV. The
CC   antibodies or antigens of HBV genotype G are useful for identifying a
CC   stage of liver disease caused by HBV genotype G. The present sequence is
CC   a hepatitis B virus (HBV) strain FR1, genotype G DNA fragment encoding e
CC   antigen (HBeAg)
XX
SQ   Sequence 87 BP; 14 A; 24 C; 17 G; 32 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 4;  Length 87;
  Best Local Similarity  100.0%;  Pred. No. 6.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 12
AAD09093/c
ID   AAD09093 standard; DNA; 129 BP.
XX
AC   AAD09093;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Hepatitis B virus FR1 strain genotype G DNA fragment #1.
XX
KW   HBV genotype G; precore; HBpol; polymerase; envelope protein; preS1;
KW   preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease;
KW   hepatitis; liver cancer; HBcAg; core antigen; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200138498-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US032108.
XX
PR   24-NOV-1999;   99US-0167206P.
XX
PA   (PHAR-) PHARMASSET INC.
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Schinazi R,  De Gendt S,  Van Geyt C,  Zoulim F,  Fried M;
PI   Rossau R;
XX
DR   WPI; 2001-367676/38.
XX
PT   Novel hepatitis B virus genotype G, nucleic acids encoding virus,
PT   polypeptides encoded by nucleic acids, useful for preparing vaccine to
PT   treat or prevent the hepatitis B virus genotype G infection in a subject.
XX
PS   Claim 5; Page 57; 84pp; English.
XX
CC   The present invention relates to hepatitis B virus (HBV) strain FR1,
CC   genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1,
CC   PreS2 and surface antigen HBsAg) and HBX proteins. HBV genotype G nucleic
CC   acids and polypeptides are useful for diagnosing, prognosing and treating
CC   infections caused by HBV genotype G. They can be used in a vaccine to
CC   treat or prevent HBV genotype G infection. The HBV genotype G derived
CC   nucleic acids and antibodies are useful for detecting HBV genotype G in a
CC   sample or diagnosis of HBV genotype G infection. The presence of HBV
CC   genotype G statistically correlates with the presence of liver damage
CC   and/or liver cancer in the subject. The HBV genotype G core insert
CC   peptide encoding nucleic acid is useful for designing monitoring assays
CC   to study and predict the evolution of anti-HBe and anti-HBc antibodies
CC   and HBeAg (genotype G e antigen) in patients infected with HBV. The
CC   antibodies or antigens of HBV genotype G are useful for identifying a
CC   stage of liver disease caused by HBV genotype G. The present sequence is
CC   a hepatitis B virus (HBV) strain FR1, genotype G DNA fragment
XX
SQ   Sequence 129 BP; 25 A; 32 C; 26 G; 46 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 4;  Length 129;
  Best Local Similarity  100.0%;  Pred. No. 7.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 13
ABK29867/c
ID   ABK29867 standard; DNA; 250 BP.
XX
```

```
AC   ABK29867;
XX
DT   23-APR-2002  (first entry)
XX
DE   Wild type hepatitis B virus core promoter.
XX
KW   Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
KW   HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
KW   vanH promoter; androgen receptor promoter; AR promoter;
KW   human epidermal growth factor receptor 2 promoter; her2 promoter;
KW   beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
KW   colon cancer; immunological disorder; prostate cancer; cytostatic;
KW   autoimmune disease; HBV pre-S promoter; HBV-X promoter;
KW   Enterococcus infection; immunosuppressive; antibacterial; antiviral;
KW   gene expression modulator; multiple sclerosis; MS;
KW   chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
KW   systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
KW   familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
KW   transgenic; ds.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    61. .72
FT                   /*tag=  a
FT                   /bound_moiety= "HNF4"
FT                   /note= "Hepatocyte nuclear factor 4"
FT   misc_binding    80. .90
FT                   /*tag=  b
FT                   /bound_moiety= "HNF3-1"
FT                   /note= "Hepatocyte nuclear factor 3-1"
FT   misc_binding    115. .126
FT                   /*tag=  c
FT                   /bound_moiety= "HNF3-2"
FT                   /note= "Hepatocyte nuclear factor 3-2"
XX
PN   WO200194600-A2.
XX
PD   13-DEC-2001.
XX
PF   06-JUN-2001; 2001WO-US018343.
XX
PR   06-JUN-2000; 2000US-0209549P.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Kim JP,  Starr DB,  Tam AW,  Laurance ME,  Michelotti EF;
PI   Velligan MD,  Latour DR,  Thomas RL,  Kongpachith A,  Sheppard LT;
PI   Lim MY,  Bruice TW;
XX
DR   WPI; 2002-130595/17.
XX
PT   New nucleic acid regulatory sequences, which are able to regulate
PT   expression of a gene operably linked to a promoter, useful for regulating
PT   the expression of transgenes and for treating e.g., cancer and
PT   immunological diseases.
XX
PS   Disclosure; Fig 1A; 95pp; English.
XX
CC   The invention describes an isolated nucleic acid regulatory sequence for
CC   a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
CC   (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
CC   epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
CC   (Bla) promoter. Transcription regulatory sequences may be used to
CC   regulate expression of the endogenous, autologous or heterologous genes
CC   operably linked to the promoter, and may be incorporated into
CC   heterologous nucleic acid constructs for use in regulated expression of
CC   transgenes. Regulated expression of cyclin D1 can be used in cancer
CC   therapies, such as breast, colon or pancreatic cancers and familial
CC   adenomatous polyposis. Regulation of the activity of CD40L gene promoter
CC   may be used in the treatment of immunological disorders, such as
CC   autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
CC   erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
CC   arthritis. Regulated expression of genes under the control of the HBV
CC   (hepatitis B)-specific core, pre-S and X promoters can be used in the
CC   therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
CC   hepatocellular carcinoma, and in the regulated expression of liver cell-
CC   specific genes. Regulated expression of the vanH gene promoter can be
CC   used in treatment of Enterococcus infection, while regulated expression
CC   of the androgen receptor gene can be used in the treatment of prostate
CC   cancer. This sequence represents the hepatitis B virus core promoter the
CC   regulatory regions of which are described in the method of the invention
XX
SQ   Sequence 250 BP; 66 A; 59 C; 62 G; 63 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        248 AGAGATGATTAGGCAGAGGT 229


RESULT 14
AAD27422/c
ID   AAD27422 standard; DNA; 639 BP.
XX
AC   AAD27422;
XX
DT   18-APR-2002  (first entry)
XX
DE   Hepatitis B virus (HBV) core antigen (HBcAg) encoding DNA #1.
XX
KW   Hepatitis B virus; HBV; core antigen; HBcAg; immune system; typhoid;
KW   prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes;
KW   hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea;
KW   tuberculosis; polio; rabies; acquired immunodeficiency syndrome; AIDS;
KW   dengue fever; yellow fever; malaria; whooping cough; salmonellosis;
KW   food poisoning; meningitis; gonorrhea; antiviral; antibacterial;
KW   antiprotozoal; ds.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .639
FT                   /*tag=  a
FT                   /product= "HBcAg"
XX
PN   WO200198333-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-GB002817.
XX
PR   22-JUN-2000; 2000GB-00015308.
PR   06-OCT-2000; 2000GB-00024544.
XX
PA   (CELL-) CELLTECH PHARM LTD.
XX
PI   Page M,  Li J,  Pumpens P;
XX
DR   WPI; 2002-098223/13.
DR   P-PSDB; AAE17018.
XX
PT   New proteins comprising a modified hepatitis B core antigen, useful as a
PT   vaccine in prophylactic or therapeutic vaccination of the human or animal
PT   body, particularly against hepatitis B virus infection.
XX
PS   Disclosure; Page 38-39; 40pp; English.
XX
CC   The invention relates to modified proteins comprising hepatitis B virus
CC   (HBV) core antigen (HBcAg) wherein one or more of the four arginine
CC   repeats has been deleted and the protein comprising the C-terminal
CC   cysteine of HBcAg. The deleted region may be replaced by an epitope from
CC   a protein other than HBcAg, in which case the HBcAg acts as a carrier to
```

CC present the epitope to the immune system. This chimeric protein or its
CC nucleic acid is useful as a vaccine or in a method of prophylactic or
CC therapeutic vaccination of the human or animal body, particularly against
CC HBV. The nucleic acid encoding the protein may be used in gene therapy or
CC DNA vaccination protocols. The chimeric protein or its nucleic acid may
CC also be used as the basis of a prophylactic vaccine against a range of
CC diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV),
CC influenza, foot-and-mouth disease, polio, herpes, rabies, acquired
CC immunodeficiency syndrome (AIDS), dengue fever, yellow fever, malaria,
CC tuberculosis, whooping cough, salmonellosis, typhoid, food poisoning,
CC diarrhoea, meningitis or gonorrhea. The present sequence is a DNA
CC encoding Hepatitis B virus core antigen (HBcAg)
XX
SQ Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 639;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 33 AGAGATGATTAGGCAGAGGT 14

RESULT 15
AAD31509/c
ID AAD31509 standard; DNA; 639 BP.
XX
AC AAD31509;
XX
DT 18-JUN-2002 (first entry)
XX
DE Hepatitis B virus core antigen (HBcAg) encoding DNA.
XX
KW Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis;
KW therapeutic; vaccine; acquired immune deficiency syndrome; influenza;
KW polio; herpes; rabies; AIDS; foot-and-mouth disease; ds.
XX
OS Hepatitis B virus.
XX
FH Key Location/Qualifiers
FT CDS 1. .639
FT /*tag= a
FT /product= "HBc protein"
FT sig_peptide 1. .87
FT /*tag= b
FT mat_peptide 88. .636
FT /*tag= c
FT /product= "Mature HBc protein"
XX
PN WO200177158-A1.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-GB001607.
XX
PR 07-APR-2000; 2000EP-00107118.
XX
PA (MEDE-) MEDEVA EURO LTD.
XX
PI Gehin A, Gilbert R, Stuart D, Rowlands D;
XX
DR WPI; 2002-239995/29.
DR P-PSDB; AAE19793.
XX
PT Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for the
PT prophylactic or therapeutic treatment of humans or animals against e.g.
PT HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-and-
PT mouth disease.
XX
PS Disclosure; Page 23-24; 27pp; English.
XX
CC The present invention relates to hepatitis B virus (HBV) core antigen
CC (HBcAg) fusion proteins and polynucleotides encoding such proteins.
CC Sequences of the invention are useful in methods of prophylactic or
CC therapeutic vaccination or to manufacture medicaments for prophylactic or
CC therapeutic vaccination of the human or animal body against HBV, e.g.
CC against viral hepatitis. They are also useful as a prophylactic vaccine
CC against e.g. hepatitis c virus, influenza, polio, herpes, rabies,
CC acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The
CC present sequence is a DNA encoding hepatitis B virus core antigen (HBcAg)
XX
SQ Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 639;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 33 AGAGATGATTAGGCAGAGGT 14

RESULT 16
ADL56756/c
ID ADL56756 standard; DNA; 646 BP.
XX
AC ADL56756;
XX
DT 17-JUN-2004 (first entry)
XX
DE HBV precore/core DNA.
XX
KW ds; precore/core; cancer; genetic disease; arthritis; AIDS.
XX
OS Hepatitis B virus.
XX
PN US2004063652-A1.
XX
PD 01-APR-2004.
XX
PF 29-MAR-2001; 2001US-00821662.
XX
PR 21-MAR-1988; 88US-00170515.
PR 18-AUG-1989; 89US-00395932.
PR 10-AUG-1990; 90US-00565606.
PR 21-SEP-1990; 90US-00586603.
PR 29-NOV-1991; 91US-00800328.
PR 04-FEB-1992; 92US-00830417.
PR 22-OCT-1992; 92US-00965084.
PR 17-MAR-1993; 93US-00032385.
PR 04-AUG-1993; 93US-00102132.
PR 09-AUG-1993; 93US-00104424.
PR 15-SEP-1993; 93US-00122791.
PR 18-NOV-1993; 93US-00155944.
PR 25-NOV-1997; 97US-00978293.
XX
PA (JOLL/) JOLLY D J.
PA (MONT/) MONTISANO D.
XX
PI Jolly DJ, Montisano D;
XX
DR WPI; 2004-282522/26.
XX
PT Introducing nucleic acid molecules to an animal or human, useful for
PT treating diseases including cancer, genetic diseases, arthritis or AIDS
PT comprises administering a composition comprising two or more gene
PT delivery vehicles.
XX
PS Disclosure; SEQ ID NO 23; 72pp; English.
XX
CC The invention relates to a method of introducing nucleic acid molecules
CC to an animal which comprises administering a composition comprising two
CC or more gene delivery vehicles to an animal at the same time and same
CC site via a single administration device. The method is useful for
CC introducing nucleic acid molecules to an animal, preferably humans for

```
CC   treating diseases including cancer, genetic diseases, arthritis or AIDS.
CC   The method can also be administered to plants using traditional methods.
CC   The introduction of multiple or more than one nucleic acid molecule at
CC   one time provide significant advantages because multiple nucleic acid
CC   molecules can provide complementary substances or activities to a single
CC   organ or joint. The difficulty, cost and time to engineer multiple
CC   nucleic acid molecules is much less than engineering a single molecule.
CC   With the use of multiple molecules, there is less chance that one
CC   substance or activity will sterically hinder or otherwise interfere with
CC   another substance or activity. The use of multiple molecules also permits
CC   the expression of different substances or activities from expression
CC   systems subject to differing activating events, thus permitting better
CC   control of differential expression of the different substances or
CC   activities. The present sequence represents the HBV precore/core DNA.
XX
SQ   Sequence 646 BP; 154 A; 170 C; 137 G; 185 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 12;  Length 646;
  Best Local Similarity  100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 17
AAQ47014/c
ID   AAQ47014 standard; DNA; 655 BP.
XX
AC   AAQ47014;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   31-JAN-1994  (first entry)
XX
DE   HBV (adw) corrected precore/core sequence.
XX
KW   Precore; core; coding region; hepatitis B; virus; HBV; plasmid; KSII+;
KW   KSII+HBpc/c; pAM6; deletion; frameshift; PCR; overlap extension; SK+ HBe;
KW   primers; mutation; hepatocellular carcinomas; class-I;
KW   cytotoxic T-lymphocyte; CTL; hepatitis C; infection; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   mutation        334
FT                   /*tag=  a
FT                   /note= "Nucleotide which is deleted in plasmid pAM6"
XX
PN   WO9315207-A2.
XX
PD   05-AUG-1993.
XX
PF   04-FEB-1993;   93WO-US001009.
XX
PR   04-FEB-1992;   92US-00830417.
XX
PA   (VIAG-) VIAGENE INC.
XX
PI   Jolly DJ,  Chang SMW,  Lee WT,  Townsend K,  Odea J;
XX
DR   WPI; 1993-258682/32.
XX
PT   Treatment of hepatitis B and C, and associated carcinoma(s) - using a
PT   vector construct directing the expression of part of hepatitis B or C
PT   antigen.
XX
PS   Example 2; Fig 2; 110pp; English.
XX
CC   This sequence represents the entire precore/core coding region of
CC   hepatitis B virus (HBV) isolated from the plasmid KSII+HBpc/c. This
CC   plasmid was created by ligating a 1.8 kb fragment of plasmid pAM6
CC   containing the entire precore/core region, into the BamHI site of KSII+.
CC   The precore/core region of plasmid KSII+HBpc/p was sequenced and was
CC   found to contain a single base pair deletion which causes a frameshift at
CC   codon 79 which results in two consecutive in-frame TAG codons. This
CC   deletion was corrected by PCR overlap extension in plasmid SK+ HBe using
CC   the primer sequences given in AAQ47015-18 in four separate reactions. The
CC   mutation may also be corrected using the primers given in AAQ47019-23 in
CC   a separate series of reactions. The isolated HBV precore/core region may
CC   be used in a method to induce potent class-I restricted protective and
CC   therapeutic cytotoxic T-lymphocyte (CTL) response, and a humoral response
CC   for the treatment of hepatitis B and C infections, as well as
CC   hepatocellular carcinomas. (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 2;  Length 655;
  Best Local Similarity  100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 18
AAT35649/c
ID   AAT35649 standard; cDNA; 655 BP.
XX
AC   AAT35649;
XX
DT   27-AUG-2003  (revised)
DT   25-FEB-1997  (first entry)
XX
DE   Precore/core region of HBV.
XX
KW   Precore; core region; HBV; hepatitis B virus; gene delivery vehicle; GDV;
KW   immunogen; HBV antigen; hepatitis C carcinoma cell; HBV infection;
KW   gene expression; non-tumourigenic tumour associated antigen; therapy;
KW   altered ras gene; altered p53 gene; altered mucin; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    10. .97
FT                   /*tag=  a
FT                   /note= "precore region"
FT   misc_feature    98. .655
FT                   /*tag=  b
FT                   /note= "core region"
XX
PN   WO9621015-A2.
XX
PD   11-JUL-1996.
XX
PF   22-DEC-1995;   95WO-US016964.
XX
PR   30-DEC-1994;   94US-00368210.
XX
PA   (CHIR ) CHIRON VIAGENE INC.
XX
PI   Jolly DJ,  Montisano D;
XX
DR   WPI; 1996-333990/33.
XX
PT   Introduction of nucleic acid molecules to an animal - comprises
PT   administration of two or more gene delivery vehicles comprising
PT   heterologous nucleic acid.
XX
PS   Disclosure; Page 131; 161pp; English.
XX
CC   This sequence represents the precore/core region of the hepatitis B virus
CC   (HBV) genome. This sequence can be included in a gene delivery vehicle
```

CC (GDV) of the invention, and is used as an immunogenic portion of a HBV
CC antigen. The GDVs can be used in the method of the invention, for
CC introducing nucleic acids into an animal, by administration of a
CC composition comprising two or more GDVs, in combination with a carrier or
CC diluent. Each GDV contains a nucleic acid molecule not naturally
CC contained within the GDV, or directs expression of at least one substance
CC (or biologically active nucleic acid) in host cells containing the GDV.
CC The two GDVs collectively direct the expression of at least two different
CC substances, or direct the expression of at least one substance, where the
CC GDVs differ in one or more biological functions. The GDVs can be used for
CC destroying hepatitis C carcinoma cells, for treating HBV (when a GDV
CC contains an immunogenic HBV fragment such as this sequence). The GDVs can
CC also be used for directing expression of non-tumourigenic, tumour
CC associated antigens (such as altered ras gene), altered p53 gene, and
CC altered mucin. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 655;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 43 AGAGATGATTAGGCAGAGGT 24

RESULT 19
AAH77569/c
ID AAH77569 standard; DNA; 655 BP.
XX
AC AAH77569;
XX
DT 19-OCT-2001 (first entry)
XX
DE HBV genotype G strain US1 preCore/Core DNA.
XX
KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW HBeAg; ds.
XX
OS Hepatitis B virus.
XX
PN WO200140279-A2.
XX
PD 07-JUN-2001.
XX
PF 20-NOV-2000; 2000WO-EP011526.
XX
PR 03-DEC-1999; 99EP-00870252.
PR 07-DEC-1999; 99US-0169287P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Van Geyt C, De Gendt S;
XX
DR WPI; 2001-374785/39.
XX
PT Novel isolated and/or purified hepatitis B virus polypeptide and
PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT therapy.
XX
PS Claim 3; Fig 7; 94pp; English.
XX
CC The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC This genotype was found with a high prevalence in patients chronically
CC infected with HBV and residing in Europe and the USA. The invention
CC relates to a fully defined sequence of 3248 nucleotides as given in
CC specification, a sequence with 92% identity to the given sequence, or
CC sequence that is degenerate to the mentioned sequences. These
CC polynucleotides are useful for HBV genotyping. The proteins encoded by
CC the polynucleotides are useful for detecting antibodies in a biological
CC sample. Ligands that bind to the proteins and antibodies directed against
CC the proteins are useful for detecting the proteins and for detecting
CC HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC preparing a vaccine or medicament for treating HBV infections. The
CC present sequence is provided in an alignment of preCore/Core sequences of
CC an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC US6, US7, US9, US10) of HBV genotype G
XX
SQ Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

Query Match 100.0%; Score 20; DB 4; Length 655;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 33 AGAGATGATTAGGCAGAGGT 14

RESULT 20
AAH77568/c
ID AAH77568 standard; DNA; 655 BP.
XX
AC AAH77568;
XX
DT 19-OCT-2001 (first entry)
XX
DE HBV genotype G strain FR2 preCore/Core DNA.
XX
KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW HBeAg; ds.
XX
OS Hepatitis B virus.
XX
PN WO200140279-A2.
XX
PD 07-JUN-2001.
XX
PF 20-NOV-2000; 2000WO-EP011526.
XX
PR 03-DEC-1999; 99EP-00870252.
PR 07-DEC-1999; 99US-0169287P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Van Geyt C, De Gendt S;
XX
DR WPI; 2001-374785/39.
XX
PT Novel isolated and/or purified hepatitis B virus polypeptide and
PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT therapy.
XX
PS Claim 3; Fig 7; 94pp; English.
XX
CC The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC This genotype was found with a high prevalence in patients chronically
CC infected with HBV and residing in Europe and the USA. The invention
CC relates to a fully defined sequence of 3248 nucleotides as given in
CC specification, a sequence with 92% identity to the given sequence, or
CC sequence that is degenerate to the mentioned sequences. These
CC polynucleotides are useful for HBV genotyping. The proteins encoded by
CC the polynucleotides are useful for detecting antibodies in a biological
CC sample. Ligands that bind to the proteins and antibodies directed against
CC the proteins are useful for detecting the proteins and for detecting
CC HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC preparing a vaccine or medicament for treating HBV infections. The
CC present sequence is provided in an alignment of preCore/Core sequences of
CC an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,

```
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 21
AAH77574/c
ID   AAH77574 standard; DNA; 655 BP.
XX
AC   AAH77574;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US10 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 22
AAH77573/c
ID   AAH77573 standard; DNA; 655 BP.
XX
AC   AAH77573;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US7 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 23
```

```
AAH77570/c
ID   AAH77570 standard; DNA; 655 BP.
XX
AC   AAH77570;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US3 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 24
AAH77571/c
ID   AAH77571 standard; DNA; 655 BP.
XX
AC   AAH77571;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US5 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 138 A; 154 C; 140 G; 195 T; 0 U; 28 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 25
AAD21244/c
ID   AAD21244 standard; DNA; 655 BP.
XX
AC   AAD21244;
XX
DT   15-JAN-2002  (first entry)
XX
DE   Hepatitis B virus adw strain precore/core mutant DNA.
XX
KW   Hepatitis B; hepatitis C; immunogen; HBV; HCV; hepatocellular carcinoma;
KW   HCC; gene therapy; virucide; hepatotropic; antiinflammatory; cytostatic;
KW   mutant; ds.
XX
OS   Hepatitis B virus.
```

```
XX
FH   Key             Location/Qualifiers
FT   misc_feature    11. .97
FT                   /*tag=  a
FT                   /note= "Precore region"
FT   misc_feature    98. .655
FT                   /*tag=  b
FT                   /note= "Core region"
FT   mutation        replace(332. .334, CC)
FT                   /*tag=  c
FT   mutation        replace(338. .340, CAA)
FT                   /*tag=  d
XX
PN   US6297048-B1.
XX
PD   02-OCT-2001.
XX
PF   07-JUN-1995;   95US-00483511.
XX
PR   04-FEB-1992;   92US-00830417.
PR   17-MAR-1993;   93US-00032385.
PR   04-AUG-1993;   93US-00102132.
PR   05-AUG-1994;   94US-00286829.
PR   19-JAN-1995;   95US-00374414.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Chang SMW,  Lee WTL,  Townsend K,  O'dea J;
XX
DR   WPI; 2001-647290/74.
XX
PT   New vectors that direct the (co-)expression of one or more immunogenic
PT   portions of the hepatitis B or C virus antigen(s), useful in gene
PT   therapy, e.g. for treating or preventing hepatitis B or C infections, or
PT   hepatocellular carcinomas.
XX
PS   Example 2; Fig 2; 64pp; English.
XX
CC   The present invention relates to a method for treating hepatitis B or C
CC   infections. The method involves administering a vector construct that
CC   directs the expression of at least one immunogenic portion of hepatitis B
CC   virus (HBV) antigen, containing HBeAg, HbcAg, HbsAg, S, Pre-S1, Pre-S2,
CC   open reading frame (ORF) 5, ORF 6, HBV pol or HBxAg or co-expression of
CC   at least one immunogenic portion of a HBV antigen and at least one
CC   immunogenic portion of a hepatitis C virus (HCV) antigen. The vectors are
CC   useful in gene therapy, particularly for treating or preventing hepatitis
CC   B and hepatitis C infections, as well as hepatocellular carcinomas (HCC).
CC   The present sequence is a PCR primer used for amplifying Hepatitis B
CC   virus adw strain precore/core mutant DNA
XX
SQ   Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 26
ABX80077/c
ID   ABX80077 standard; DNA; 655 BP.
XX
AC   ABX80077;
XX
DT   22-APR-2003  (first entry)
XX
DE   Hepatitis B virus precore/core DNA.
XX
KW   Hepatitis B virus; hepatitis C virus; hepatitis C infection; poliovirus;
KW   hepatitis B infection; hepatitis C antigen; polyprotein antigen; SV40;
KW   rhinovirus; pox virus; canary pox virus; vaccinia virus; influenza virus;
KW   adenovirus; parvovirus; adeno-associated virus; herpes virus; measles;
KW   corona virus; HIV; human immunodeficiency virus; Sindbis virus; virucide;
KW   hepatotropic; ds; precore/core DNA.
XX
OS   Hepatitis B virus.
XX
PN   US2002141974-A1.
XX
PD   03-OCT-2002.
XX
PF   24-JUL-2001; 2001US-00912679.
XX
PR   04-FEB-1992;   92US-00830417.
PR   17-MAR-1993;   93US-00032385.
PR   04-AUG-1993;   93US-00102132.
PR   05-AUG-1994;   94US-00286829.
PR   19-JAN-1995;   95US-00374414.
PR   07-JUN-1995;   95US-00483511.
XX
PA   (JOLL/) JOLLY D J.
PA   (CHAN/) CHANG S M W.
PA   (LEEW/) LEE W T L.
PA   (TOWN/) TOWNSEND K.
PA   (ODEA/) O'DEA J.
XX
PI   Jolly DJ,  Chang SMW,  Lee WTL,  Townsend K,  O'dea J;
XX
DR   WPI; 2003-174125/17.
XX
PT   Treating hepatitis C infections in a warm-blooded animal by administering
PT   a vector construct, which directs the expression of an immunogenic
PT   portion of a hepatitis C antigen, and alternatively, with an
PT   immunomodulatory cofactor.
XX
PS   Example 2; Fig 2; 70pp; English.
XX
CC   The invention relates to a method for treating hepatitis C infections in
CC   a warm-blooded animal comprising administering a vector construct which
CC   directs the expression of at least one immunogenic portion of a hepatitis
CC   C antigen, where an immune response is generated, and alternatively, in
CC   combination with an immunomodulatory cofactor. The invention also relates
CC   to a vector construct which directs the co-expression of at least one
CC   immunogenic portion of a hepatitis B antigen and at least one immunogenic
CC   portion of a hepatitis C antigen, an immunogenic portion of the
CC   polyprotein antigen, or an immunogenic portion of the polyprotein antigen
CC   and an immunoregulatory cofactor. A recombinant virus carrying the vector
CC   construct is selected from poliovirus, rhinovirus, pox virus, canary pox
CC   virus, vaccinia virus, influenza virus, adenovirus, parvovirus, adeno-
CC   associated virus, herpes virus, SV40, HIV, measles, corona virus or
CC   Sindbis virus. This sequence represents hepatitis B virus precore/core
CC   DNA used in the method of the invention
XX
SQ   Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 9;  Length 655;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 27
ABX96938/c
ID   ABX96938 standard; DNA; 655 BP.
XX
AC   ABX96938;
XX
DT   15-MAY-2003  (first entry)
XX
DE   Hepatitis B virus (HBV) DNA.
```

```
XX
KW   Human; HBV; HCV; gene; ds; hepatitis B virus; hepatitis C virus;
KW   intracellular infection; HSV; HIV; viral infection; herpes simplex virus;
KW   human immunodeficiency virus; FIV; feline immunodeficiency virus;
KW   parasitic infection; rickettsia; malaria; leishmaniasis; tuberculosis;
KW   bacterial disease; legionella; chlamydia.
XX
OS   Hepatitis B virus.
XX
PN   US2002165172-A1.
XX
PD   07-NOV-2002.
XX
PF   17-DEC-1999;   99US-00466035.
XX
PR   16-SEP-1997;   97US-00931031.
XX
PA   (SALL/) SALLBERG M.
PA   (MILI/) MILICH D R.
PA   (LEEW/) LEE W T L.
XX
PI   Sallberg M,  Milich DR,  Lee WTL;
XX
DR   WPI; 2003-288144/28.
XX
PT   Treating intracellular infections, e.g. viral, parasitic and bacterial
PT   diseases, comprises administering a vector construct which directs the
PT   expression of an immunogenic portion of an antigen from an intracellular
PT   pathogen.
XX
PS   Disclosure; Page 44-45; 69pp; English.
XX
CC   The invention relates to a method for treating intracellular infections
CC   within warm-blooded animals comprising administering to a warm-blooded
CC   animal a vector construct which directs the expression of at least one
CC   immunogenic portion of an antigen derived from an intracellular pathogen,
CC   and a protein having the immunogenic portion of the antigen to generate
CC   an immune response. The method is useful for treating intracellular
CC   infections or diseases including viral infections (e.g. hepatitis B virus
CC   (HBV), hepatitis C virus (HCV), herpes simplex virus (HSV), human
CC   immunodeficiency virus (HIV) or feline immunodeficiency virus (FIV)),
CC   parasitic infections (e.g. rickettsia, leishmaniasis or malaria) and
CC   certain bacterial diseases (e.g. legionella, tuberculosis or chlamydia).
CC   This sequence represents hepatitis B virus DNA used in the method of the
CC   invention
XX
SQ   Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 10;  Length 655;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 28
AAN91081/c
ID   AAN91081 standard; DNA; 660 BP.
XX
AC   AAN91081;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1990  (first entry)
XX
DE   DNA sequence of subclones encompassing the core (C) and precore (preC)
DE   antigens (Ag) of an adw serotype hepatitis B (HB) virus.
XX
KW   Hepatitis B virus; core gene; precore gene; antigen; vaccine;
KW   polypeptide expression sequence; AcNPV transfer vector pAcYM1;
KW   pAcYM1KTpc; pAcYM1KTc; recombinant baculovirus; YM1KYpc; MY1KTc.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .658
FT                   /*tag=  e
FT   misc_feature    2. .100
FT                   /*tag=  c
FT                   /note= "This is labelled 'preCore'"
FT   CDS             14. .82
FT                   /*tag=  a
FT                   /product= "Precore antigen"
FT   misc_feature    83. .659
FT                   /*tag=  d
FT                   /note= "This labelled 'Core'"
FT   CDS             101. .658
FT                   /*tag=  b
FT                   /product= "Core Antigen"
FT   conflict        169
FT                   /*tag=  f
FT                   /note= "Differs from the HB virus adw sequence published
FT                   by Ono and associates (1983)"
FT   conflict        181. .182
FT                   /*tag=  g
FT                   /note= "As above"
FT   conflict        217
FT                   /*tag=  h
FT                   /note= "As above"
FT   conflict        274
FT                   /*tag=  i
FT                   /note= "As above"
FT   conflict        329
FT                   /*tag=  j
FT                   /note= "As above"
FT   conflict        346
FT                   /*tag=  k
FT                   /note= "As above"
XX
PN   WO8901518-A.
XX
PD   23-FEB-1989.
XX
PF   11-AUG-1988;   88WO-GB000663.
XX
PR   12-AUG-1987;   87GB-00019108.
PR   12-JUL-1988;   88GB-00016084.
XX
PA   (NATU-) NATURAL ENVIRON RES.
XX
PI   Bishop DH,  Emery VC;
XX
DR   WPI; 1989-068873/09.
DR   P-PSDB; AAP90702.
XX
PT   New plasmid replicon for inserting several genes into vector - contg. two
PT   polypeptide expression structures, and derived viral vectors for
PT   infecting insect cells.
XX
PS   Disclosure; Page ?; 74pp; English.
XX
CC   The coding sequences of the preC and C Ags of HB virus were inserted into
CC   Autograph californica nuclear polyhedrosis virus (AcNPV) transfer vector
CC   pAcYM1. The derived recombinant transfer vectors were called pAcYM1KTpc
CC   and pAcYM1KTc. Following cotransfection with infectious AcNPV DNA,
CC   recombinant baculoviruses were obtained - YM1KYc and YM1KYpc. It was
CC   determined that all the HBcAg and HBpcAg was cell associated and that the
CC   yield of purified HBcAg was of the order of 5 mg per liter of 1x10(9)
CC   infected cells. Such Ag may be useful in vaccines. (Updated on 25-MAR-
CC   2003 to correct PR field.)
XX
SQ   Sequence 660 BP; 156 A; 171 C; 143 G; 189 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
```

```
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         46 AGAGATGATTAGGCAGAGGT 27


RESULT 29
AAH77572/c
ID   AAH77572 standard; DNA; 664 BP.
XX
AC   AAH77572;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US6 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 664 BP; 146 A; 160 C; 144 G; 208 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 664;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 30
ADO07220/c
ID   ADO07220 standard; DNA; 669 BP.
XX
AC   ADO07220;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Hepatitis B virus core antigen DNA.
XX
KW   HBcAg; immunomodulator; vaccine; gene; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             10. .669
FT                   /*tag=  a
FT                   /product= "HBcAg"
FT                   /partial
FT                   /note= "No start codon"
XX
PN   WO2004035007-A2.
XX
PD   29-APR-2004.
XX
PF   17-OCT-2003; 2003WO-US033178.
XX
PR   17-OCT-2002; 2002US-0419279P.
XX
PA   (ORAG-) ORAGEN CORP.
XX
PI   Michaels F;
XX
DR   WPI; 2004-348329/32.
DR   P-PSDB; ADO07221.
XX
PT   Modulating a systemic immune response to a peptide in a mammal comprises
PT   transmucosally administering a macromolecular aggregate of the peptide.
XX
PS   Disclosure; SEQ ID NO 1; 81pp; English.
XX
CC   The present sequence is the DNA sequence of the hepatitis B virus core
CC   antigen (HBcAg) gene from HBV serotype ayw. A peptide comprising a HBV
CC   protein can be used in claimed methods of the invention for modulating an
CC   immune response in a mammal. A method of inducing a systemic immune
CC   response to a peptide in a mammal comprises transmucosally administering
CC   to the mammal a macromolecular aggregate of the peptide. The
CC   macromolecular aggregate comprises at least 10 peptide subunits, may have
CC   a molecular weight of over 1,000 kDa, and is preferably at least 5 nm in
CC   diameter. It is resistant to digestive degradation, being stabilised in
CC   aggregate form by chemical treatment and/or by recombinant protein
CC   engineering of the peptide. The peptide preferably comprises a HBV
CC   protein selected from HBV surface protein, nucleocapsid protein or
CC   envelope protein. Transmucosal administration to a mammal of a
CC   macromolecular aggregate of a HBV surface protein engenders a systemic
CC   immune response in the mammal. A method of suppressing an immune response
CC   in a mammal involves transmucosally administering a monomolecular peptide
CC   that is resistant to digestive degradation and which may be stabilised by
CC   chemical treatment or protein engineering, and which may be derived from
CC   a HBV protein. A monomolecular peptide is useful for the induction of
CC   oral tolerance when induction of systemic immunity is undesirable, e.g.
CC   in cases of chronic infections.
XX
SQ   Sequence 669 BP; 155 A; 170 C; 148 G; 196 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 12;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         63 AGAGATGATTAGGCAGAGGT 44
```

```
RESULT 31
AAD09092/c
ID   AAD09092 standard; DNA; 673 BP.
XX
AC   AAD09092;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Hepatitis B virus FR1 strain genotype G PreCore/HBcAg DNA.
XX
KW   HBV genotype G; precore; HBpol; polymerase; envelope protein; preS1;
KW   preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease;
KW   hepatitis; liver cancer; HBcAg; core antigen; ds.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .672
FT                   /*tag=  a
FT                   /product= "PreCore/HBcAg core protein"
FT                   /transl_except= (pos:4. .6, aa:Xaa)
FT                   /transl_except= (pos:82. .84, aa:Xaa)
FT                   /note= "Xaa corresponds to in-frame stop codon; Does not
FT                   include stop codon"
FT                   /partial
FT   misc_feature    1. .87
FT                   /*tag=  b
FT                   /note= "PreCore protein DNA"
FT   misc_feature    88. .672
FT                   /*tag=  c
FT                   /note= "HBcAg core protein DNA"
FT   misc_feature    94. .129
FT                   /*tag=  d
FT                   /note= "Core insert peptide DNA"
XX
PN   WO200138498-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US032108.
XX
PR   24-NOV-1999;   99US-0167206P.
XX
PA   (PHAR-) PHARMASSET INC.
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Schinazi R,  De Gendt S,  Van Geyt C,  Zoulim F,  Fried M;
PI   Rossau R;
XX
DR   WPI; 2001-367676/38.
DR   P-PSDB; AAE04707.
XX
PT   Novel hepatitis B virus genotype G, nucleic acids encoding virus,
PT   polypeptides encoded by nucleic acids, useful for preparing vaccine to
PT   treat or prevent the hepatitis B virus genotype G infection in a subject.
XX
PS   Claim 4; Page 56-57; 84pp; English.
XX
CC   The present invention relates to hepatitis B virus (HBV) strain FR1,
CC   genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1,
CC   PreS2 and surface antigen HBsAg) and HBX proteins. HBV genotype G nucleic
CC   acids and polypeptides are useful for diagnosing, prognosing and treating
CC   infections caused by HBV genotype G. They can be used in a vaccine to
CC   treat or prevent HBV genotype G infection. The HBV genotype G derived
CC   nucleic acids and antibodies are useful for detecting HBV genotype G in a
CC   sample or diagnosis of HBV genotype G infection. The presence of HBV
CC   genotype G statistically correlates with the presence of liver damage
CC   and/or liver cancer in the subject. The HBV genotype G core insert
CC   peptide encoding nucleic acid is useful for designing monitoring assays
CC   to study and predict the evolution of anti-HBe and anti-HBc antibodies
CC   and HBeAg (genotype G e antigen) in patients infected with HBV. The
CC   antibodies or antigens of HBV genotype G are useful for identifying a
CC   stage of liver disease caused by HBV genotype G. The present sequence is
CC   hepatitis B virus (HBV) strain FR1, genotype G DNA fragment encoding
CC   PreCore/Core antigen (HBcAg) protein
XX
SQ   Sequence 673 BP; 148 A; 165 C; 146 G; 214 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 673;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 32
AAH77563/c
ID   AAH77563 standard; DNA; 675 BP.
XX
AC   AAH77563;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV preCore/Core gene.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 4; Fig 2; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is the complete coding sequence of the HBV preCore/Core
CC   gene
XX
SQ   Sequence 675 BP; 149 A; 165 C; 147 G; 214 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 675;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14
```

RESULT 33
AAH77566/c
ID AAH77566 standard; DNA; 681 BP.
XX
AC AAH77566;
XX
DT 19-OCT-2001 (first entry)
XX
DE HBV genotype A strain HBVXCPS preCore/Core DNA.
XX
KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW HBeAg; ds.
XX
OS Hepatitis B virus.
XX
PN WO200140279-A2.
XX
PD 07-JUN-2001.
XX
PF 20-NOV-2000; 2000WO-EP011526.
XX
PR 03-DEC-1999; 99EP-00870252.
PR 07-DEC-1999; 99US-0169287P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Van Geyt C, De Gendt S;
XX
DR WPI; 2001-374785/39.
XX
PT Novel isolated and/or purified hepatitis B virus polypeptide and
PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT therapy.
XX
PS Example 2; Fig 7; 94pp; English.
XX
CC The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC This genotype was found with a high prevalence in patients chronically
CC infected with HBV and residing in Europe and the USA. The invention
CC relates to a fully defined sequence of 3248 nucleotides as given in
CC specification, a sequence with 92% identity to the given sequence, or
CC sequence that is degenerate to the mentioned sequences. These
CC polynucleotides are useful for HBV genotyping. The proteins encoded by
CC the polynucleotides are useful for detecting antibodies in a biological
CC sample. Ligands that bind to the proteins and antibodies directed against
CC the proteins are useful for detecting the proteins and for detecting
CC HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC preparing a vaccine or medicament for treating HBV infections. The
CC present sequence is provided in an alignment of preCore/Core sequences of
CC an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC US6, US7, US9, US10) of HBV genotype G
XX
SQ Sequence 681 BP; 151 A; 166 C; 139 G; 189 T; 0 U; 36 Other;

```
  Query Match             100.0%;  Score 20;  DB 4;  Length 681;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14
```

RESULT 34
AAH77567/c
ID AAH77567 standard; DNA; 681 BP.
XX
AC AAH77567;
XX
DT 19-OCT-2001 (first entry)
XX
DE HBV genotype G strain FR1 preCore/Core DNA.
XX
KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW HBeAg; ds.
XX
OS Hepatitis B virus.
XX
PN WO200140279-A2.
XX
PD 07-JUN-2001.
XX
PF 20-NOV-2000; 2000WO-EP011526.
XX
PR 03-DEC-1999; 99EP-00870252.
PR 07-DEC-1999; 99US-0169287P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Van Geyt C, De Gendt S;
XX
DR WPI; 2001-374785/39.
XX
PT Novel isolated and/or purified hepatitis B virus polypeptide and
PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT therapy.
XX
PS Claim 3; Fig 7; 94pp; English.
XX
CC The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC This genotype was found with a high prevalence in patients chronically
CC infected with HBV and residing in Europe and the USA. The invention
CC relates to a fully defined sequence of 3248 nucleotides as given in
CC specification, a sequence with 92% identity to the given sequence, or
CC sequence that is degenerate to the mentioned sequences. These
CC polynucleotides are useful for HBV genotyping. The proteins encoded by
CC the polynucleotides are useful for detecting antibodies in a biological
CC sample. Ligands that bind to the proteins and antibodies directed against
CC the proteins are useful for detecting the proteins and for detecting
CC HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC preparing a vaccine or medicament for treating HBV infections. The
CC present sequence is provided in an alignment of preCore/Core sequences of
CC an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC US6, US7, US9, US10) of HBV genotype G
XX
SQ Sequence 681 BP; 149 A; 165 C; 147 G; 214 T; 0 U; 6 Other;

```
  Query Match             100.0%;  Score 20;  DB 4;  Length 681;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14
```

RESULT 35
AAN80943/c
ID AAN80943 standard; DNA; 750 BP.
XX
AC AAN80943;
XX
DT 25-MAR-2003 (revised)
DT 19-NOV-1990 (first entry)

```
XX
DE   HBV core gene of plasmid pHBV-8.
XX
KW   Hepatitis B core antigen; virus; vaccine; immunoassay; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             31. .675
FT                   /*tag=  a
FT                   /product= "HBcAg"
XX
PN   EP272483-A.
XX
PD   29-JUN-1988.
XX
PF   25-NOV-1987;   87EP-00117370.
XX
PR   19-DEC-1986;   86US-00944645.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Andersen PR,  Mushahwar IK,  Mimms LT,  Staller JM;
XX
DR   WPI; 1988-176639/26.
DR   P-PSDB; AAP80961.
XX
PT   Polynucleotide encoding HBEAG and HBCAG immuno-reactive polypeptide -
PT   useful in immunoassays, for raising antibodies and as vaccine prods.
XX
PS   Disclosure; Page ?; 32pp; English.
XX
CC   The cloned HBV DNA can be used to engineer plasmids for HBcAg synthesis
CC   in bacteria. The DNA may be fused to a gene for beta galactosidase. The
CC   recombinant protein can be used for immuno- assays, to raise antibodies,
CC   and in vaccines. See also AAN82265 and 66. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 750 BP; 176 A; 192 C; 160 G; 222 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 750;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db         63 AGAGATGATTAGGCAGAGGT 44


RESULT 36
AAH77169/c
ID   AAH77169 standard; DNA; 909 BP.
XX
AC   AAH77169;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Regulatory and coding region of the X15 component in the X-myc construct.
XX
KW   Transgenic mouse; cancer; oncogene; bicistronic hepatitis B virus; HBV;
KW   X15-c-myc transgene; hepatocellular carcinoma; malignant liver tumour;
KW   X15; c-myc; murine; HBX; carcinogen; ds.
XX
OS   Hepatitis B virus.
XX
PN   US6274788-B1.
XX
PD   14-AUG-2001.
XX
PF   02-FEB-1999;   99US-00243282.
XX
PR   23-SEP-1998;   98IN-DE002858.
XX
PA   (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
PA   (NAIM-) NAT INST IMMUNOLOGY.
XX
PI   Kumar V,  Singh M,  Totey S,  Anand R;
XX
DR   WPI; 2002-009266/01.
XX
PT   New bicistronic hepatitis B virus (HBV) X15-c-myc transgene, useful for
PT   producing transgenic mouse model systems for human hepatocellular
PT   carcinoma, comprises HBV X15 transgene and c-myc transgene.
XX
PS   Claim 3; Fig 3; 12pp; English.
XX
CC   This polynucleotide represents the sequence of the regulatory and coding
CC   regions of the X15 component in the X-myc construct. The invention
CC   relates to a bicistronic hepatitis B virus (HBV) X15-c-myc transgene,
CC   comprising of the HBV X15 gene and c-myc gene. The myc gene is known to
CC   be an activatable oncogene. The transgene encodes a truncated HBV X15
CC   protein that has amino acids 58-154 of HBV X15 and a murine c-myc
CC   protein, respectively. A transgenic mouse containing the transgene
CC   construct is useful for screening a candidate substance (CS), to
CC   determine whether CS promotes hepatocellular carcinoma. This is
CC   determined by exposing a transgenic mouse to CS, and monitoring the mouse
CC   for the development of hepatocellular carcinoma, where an increase in the
CC   development of hepatocellular carcinoma in the transgenic mouse exposed
CC   to CS compared to the development of hepatocellular carcinoma in a
CC   transgenic mouse not exposed to CS, indicates that CS promotes
CC   hepatocellular carcinoma. The transgenic mice can be employed as a source
CC   for cell and tissue culture. The transgenic animal models comprising of
CC   the HBV X15-c-myc transgene for hepatocellular carcinoma are superior to
CC   any transgenic animal model system for hepatocellular carcinoma in that
CC   the transgenic mice develop more aggressive and accelerated onset of
CC   malignant liver tumours in all lobes causing death of the affected
CC   animals in 20-22 weeks, that is faster than the time taken by the other
CC   transgenic animals to even develop a tumour
XX
SQ   Sequence 909 BP; 210 A; 236 C; 211 G; 252 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 909;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        851 AGAGATGATTAGGCAGAGGT 832


RESULT 37
AAV82691/c
ID   AAV82691 standard; DNA; 1334 BP.
XX
AC   AAV82691;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV12 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
```

```
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1334 BP; 288 A; 363 C; 311 G; 372 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1334;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        735 AGAGATGATTAGGCAGAGGT 716


RESULT 38
AAV82688/c
ID   AAV82688 standard; DNA; 1395 BP.
XX
AC   AAV82688;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV5 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1395 BP; 277 A; 387 C; 331 G; 398 T; 0 U; 2 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 39
AAV82687/c
ID   AAV82687 standard; DNA; 1400 BP.
XX
AC   AAV82687;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV4 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
```

```
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1400 BP; 287 A; 388 C; 332 G; 393 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1400;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 40
AAV82692/c
ID   AAV82692 standard; DNA; 1445 BP.
XX
AC   AAV82692;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV13 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1445 BP; 297 A; 406 C; 338 G; 404 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1445;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 41
AAV82685/c
ID   AAV82685 standard; DNA; 1445 BP.
XX
AC   AAV82685;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV2 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1445 BP; 298 A; 393 C; 340 G; 414 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1445;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 42
AAV82690/c
ID   AAV82690 standard; DNA; 1445 BP.
XX
AC   AAV82690;
XX
DT   16-FEB-1999  (first entry)
XX
```

DE Fulminant hepatitis B virus genotype D variant FHBV7 sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations
PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1445 BP; 293 A; 402 C; 340 G; 410 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1445;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 846 AGAGATGATTAGGCAGAGGT 827

RESULT 43
AAV82684/c
ID AAV82684 standard; DNA; 1445 BP.
XX
AC AAV82684;
XX
DT 16-FEB-1999 (first entry)
XX
DE Fulminant hepatitis B virus genotype D variant FHBV1 sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations
PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1445 BP; 298 A; 400 C; 336 G; 411 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1445;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 846 AGAGATGATTAGGCAGAGGT 827

RESULT 44
AAV82695/c
ID AAV82695 standard; DNA; 1500 BP.
XX
AC AAV82695;
XX
DT 16-FEB-1999 (first entry)
XX
DE Fulminant hepatitis B virus genotype D variant CHBV2 sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations

PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1500 BP; 308 A; 412 C; 347 G; 433 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1500;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 846 AGAGATGATTAGGCAGAGGT 827

RESULT 45
AAV82683/c
ID AAV82683 standard; DNA; 1500 BP.
XX
AC AAV82683;
XX
DT 16-FEB-1999 (first entry)
XX
DE Fulminant hepatitis B virus genotype D variant AHBV1 sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations
PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1500 BP; 305 A; 411 C; 354 G; 430 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1500;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 846 AGAGATGATTAGGCAGAGGT 827

RESULT 46
AAV82694/c
ID AAV82694 standard; DNA; 1500 BP.
XX
AC AAV82694;
XX
DT 16-FEB-1999 (first entry)
XX
DE Fulminant hepatitis B virus genotype D variant HBVP2CSX sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations
PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1500 BP; 305 A; 408 C; 349 G; 438 T; 0 U; 0 Other;

```
  Query Match           100.0%;  Score 20;  DB 2;  Length 1500;
  Best Local Similarity  100.0%;  Pred. No. 9.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 47
AAV82686/c
ID   AAV82686 standard; DNA; 1500 BP.
XX
AC   AAV82686;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV3 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1500 BP; 305 A; 413 C; 353 G; 429 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 2;  Length 1500;
  Best Local Similarity  100.0%;  Pred. No. 9.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 48
AAV82706/c
ID   AAV82706 standard; DNA; 1500 BP.
XX
AC   AAV82706;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Wild type hepatitis B virus genotype D nucleotides 1000-2500.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of wild type Hepatitis
CC   B virus genotype D, nucleotides 1000 to 2500. Mutations occur in this
CC   region in fulminant hepatitis B virus (FHBV) patients. The specification
CC   describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e.
CC   alteration from the normal nucleotide in any of the genotypes A to F) in
CC   at least two of the enhancer I region, the negative regulatory element
CC   region, the enhancer II/ core upstream regulatory sequence/ basal core
CC   promoter region, or a mutation which leads to an X-peptide amino acid
CC   change to Cys or Met. The HBV variants of the invention are used to
CC   detect binding interactions between host or viral proteins and HBV
CC   nucleic acid. Probes that hybridise to any of the specified mutated
CC   regions are used to detect HBV-related disease, especially fulminant
CC   infection, but also severe chronic infection or serologically unusual
CC   forms of disease. Combinations of the specified mutations are associated
CC   with fulminant infections, probably because they reduce the ability to
CC   bind inhibitory proteins in the host cell
XX
SQ   Sequence 1500 BP; 304 A; 409 C; 351 G; 436 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 2;  Length 1500;
  Best Local Similarity  100.0%;  Pred. No. 9.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||||||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 49
AAV82689/c
ID   AAV82689 standard; DNA; 1500 BP.
XX
AC   AAV82689;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV6 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
```

KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations
PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1500 BP; 302 A; 416 C; 353 G; 427 T; 0 U; 2 Other;

Query Match 100.0%; Score 20; DB 2; Length 1500;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 846 AGAGATGATTAGGCAGAGGT 827

RESULT 50
AAV82693/c
ID AAV82693 standard; DNA; 1500 BP.
XX
AC AAV82693;
XX
DT 16-FEB-1999 (first entry)
XX
DE Fulminant hepatitis B virus genotype D variant HBVP3CSX sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations
PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1500 BP; 314 A; 403 C; 343 G; 440 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1500;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||||||||||||||
Db 846 AGAGATGATTAGGCAGAGGT 827

Search completed: December 15, 2004, 15:38:57
Job time : 185 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 15, 2004, 09:10:16 ; Search time 1339.5 Seconds
(without alignments)
544.080 Million cell updates/sec

Title: US-08-901-612A-7
Perfect score: 20
Sequence: 1 agagatgattaggcagaggt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18.4	92.0	547	4	BG487106	BG487106 dad25b04.
	2	18.4	92.0	587	5	BQ523985	BQ523985 NISC_no02
	3	18.4	92.0	612	7	CO359322	CO359322 DR_ATE_SU
	4	18.4	92.0	689	7	CN090609	CN090609 EC2BBA33C
	5	18.4	92.0	731	7	CN099540	CN099540 EC2CAA16B
	6	18.4	92.0	794	7	CO798651	CO798651 AGENCOURT
	7	18.4	92.0	859	5	BX693640	BX693640 BX693640
	8	18.4	92.0	869	7	CR417260	CR417260 CR417260
	9	18.4	92.0	886	7	CO812154	CO812154 AGENCOURT
c	10	18.4	92.0	896	7	CR445414	CR445414 CR445414
	11	18.4	92.0	910	5	BX699062	BX699062 BX699062
	12	18.4	92.0	913	5	BX683124	BX683124 BX683124
	13	18.4	92.0	914	5	BX694706	BX694706 BX694706
c	14	18	90.0	214	2	AW342249	AW342249 GthEST1 G
c	15	17.4	87.0	354	2	AW215253	AW215253 up05g04.y
	16	17.4	87.0	494	5	BQ315666	BQ315666 CM3-CT003
c	17	17.4	87.0	680	4	BG440037	BG440037 GA__Ea000
	18	17.4	87.0	741	8	BH039638	BH039638 RPCI-24-2
	19	17.4	87.0	1032	9	CNS029UK	AL187733 Tetraodon
c	20	17.4	87.0	1044	9	CNS027K3	AL184764 Tetraodon
c	21	17	85.0	248	2	BB361792	BB361792 BB361792
c	22	17	85.0	490	8	AQ355954	AQ355954 CITBI-E1-
	23	16.8	84.0	145	2	BF330446	BF330446 MR2-BN036
	24	16.8	84.0	146	2	BF330451	BF330451 MR2-BN036
	25	16.8	84.0	387	8	BZ350602	BZ350602 ht58d07.g
	26	16.8	84.0	388	1	AJ713073	AJ713073 AJ713073
c	27	16.8	84.0	407	1	AA503497	AA503497 nh59g10.s
	28	16.8	84.0	423	1	AJ572696	AJ572696 AJ572696
	29	16.8	84.0	484	9	BX975154	BX975154 Reverse s
c	30	16.8	84.0	506	2	BE558110	BE558110 fl19f03.y
	31	16.8	84.0	509	8	AZ336360	AZ336360 1M0066A09
	32	16.8	84.0	525	8	AQ317545	AQ317545 RPCI11-79
	33	16.8	84.0	526	6	CB719936	CB719936 AMGNNUC:N
	34	16.8	84.0	531	2	BE605742	BE605742 fl19f03.x
	35	16.8	84.0	533	5	BQ122423	BQ122423 EST607999
	36	16.8	84.0	537	7	CK766395	CK766395 eca01-43m
	37	16.8	84.0	558	8	AQ491131	AQ491131 RPCI-11-2
	38	16.8	84.0	568	8	AQ554673	AQ554673 RPCI-11-3
	39	16.8	84.0	599	4	BJ690447	BJ690447 BJ690447
c	40	16.8	84.0	614	9	CL186343	CL186343 104_401_1
c	41	16.8	84.0	627	8	B00642	B00642 cSRL-117e7-
	42	16.8	84.0	663	6	CD304890	CD304890 StrPu691.
	43	16.8	84.0	699	8	BH975438	BH975438 odh59a02.
c	44	16.8	84.0	707	8	BH973998	BH973998 odh10c03.
c	45	16.8	84.0	716	7	CN791475	CN791475 4126207 B
	46	16.8	84.0	718	8	AZ519049	AZ519049 RPCI-11-7
c	47	16.8	84.0	729	5	BQ782214	BQ782214 UI-R-FF0-
c	48	16.8	84.0	734	9	CL189821	CL189821 104_407_1
	49	16.8	84.0	746	8	BZ345634	BZ345634 hs87c01.b
c	50	16.8	84.0	753	9	CR100681	CR100681 Forward s
	51	16.8	84.0	757	8	BZ058489	BZ058489 lle33h12.
c	52	16.8	84.0	782	8	BZ476690	BZ476690 BONMQ75TR
	53	16.8	84.0	833	9	CC589146	CC589146 CH240_388
	54	16.8	84.0	845	9	BX975684	BX975684 Forward s
	55	16.8	84.0	876	5	BQ892054	BQ892054 AGENCOURT
c	56	16.8	84.0	909	8	AZ139209	AZ139209 SP_0174_B
	57	16.8	84.0	916	7	CO749985	CO749985 KBrAE004G
	58	16.8	84.0	924	7	CO385672	CO385672 AGENCOURT
c	59	16.8	84.0	1035	9	CNS05M70	AL343701 Tetraodon
	60	16.8	84.0	1157	5	BQ940483	BQ940483 AGENCOURT
c	61	16.8	84.0	1164	8	CC206984	CC206984 CH261-44A
	62	16.8	84.0	1170	8	CC205227	CC205227 CH261-38I
	63	16.4	82.0	176	9	CG603319	CG603319 OST277700
	64	16.4	82.0	209	6	C15694	C15694 C15694 Clon
	65	16.4	82.0	223	1	AV312932	AV312932 AV312932
c	66	16.4	82.0	268	1	AV143648	AV143648 AV143648
	67	16.4	82.0	317	7	N60556	N60556 TgESTzy15e1
	68	16.4	82.0	328	7	CF525831	CF525831 tu-c-t-54
c	69	16.4	82.0	331	2	AW771120	AW771120 hn52e09.x
c	70	16.4	82.0	400	2	BE943728	BE943728 UI-M-BH3-
	71	16.4	82.0	403	2	BE644248	BE644248 STRF005 U
	72	16.4	82.0	475	8	B40233	B40233 HS-1051-A1-
	73	16.4	82.0	483	1	AI418211	AI418211 tf75g04.x
	74	16.4	82.0	527	8	AZ775622	AZ775622 2M0008D05
	75	16.4	82.0	542	1	AI939589	AI939589 tf75g04.x
c	76	16.4	82.0	544	9	CE067804	CE067804 tigr-gss-
c	77	16.4	82.0	567	6	CB864177	CB864177 HD05E12w
	78	16.4	82.0	574	9	CE487389	CE487389 tigr-gss-
	79	16.4	82.0	585	9	CC559021	CC559021 CH240_467
c	80	16.4	82.0	589	4	BG434994	BG434994 602507263
c	81	16.4	82.0	661	6	CB864288	CB864288 HD05K05w
	82	16.4	82.0	680	9	CE792348	CE792348 tigr-gss-
c	83	16.4	82.0	692	9	AG280489	AG280489 Mus muscu
	84	16.4	82.0	694	9	CE781116	CE781116 tigr-gss-
c	85	16.4	82.0	699	8	B71004	B71004 CIT-HSP-206
	86	16.4	82.0	726	8	AZ473761	AZ473761 1M0289M18
	87	16.4	82.0	729	4	BI833319	BI833319 603087914
	88	16.4	82.0	740	7	CF788155	CF788155 856899 MA
c	89	16.4	82.0	758	9	AG359054	AG359054 Mus muscu
	90	16.4	82.0	849	9	CC586584	CC586584 CH240_383
c	91	16.4	82.0	1054	8	CC221555	CC221555 CH261-99K
c	92	16.4	82.0	1115	8	CC186082	CC186082 CH261-40D
c	93	16.4	82.0	1316	8	AQ503241	AQ503241 V43B5 mTn
	94	16.2	81.0	795	9	CNS012D3	AL101409 Drosophil
c	95	16	80.0	179	8	AQ504792	AQ504792 RPCI-11-3
c	96	16	80.0	429	9	CL428356	CL428356 ZMMBBb044
c	97	16	80.0	468	8	AQ123089	AQ123089 HS_3095_B

98	16	80.0	501	7	CN283739	CN283739 170004252
c 99	16	80.0	649	9	CC956922	CC956922 BOICH02TR
c 100	16	80.0	682	8	BH972205	BH972205 odj23g10.

ALIGNMENTS

RESULT 1
BG487106
LOCUS BG487106 547 bp mRNA linear EST 22-MAR-2001
DEFINITION dad25b04.x1 Wellcome CRC pCS107 tropicalis St10-12 Xenopus tropicalis cDNA clone IMAGE:4440511 3', mRNA sequence.
ACCESSION BG487106
VERSION BG487106.1 GI:13434683
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 547)
AUTHORS Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Xenopus EST project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 507.
FEATURES Location/Qualifiers
source 1. .547
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:4440511"
/tissue_type="whole embryo, stages 10-12"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC pCS107 tropicalis St10-12"
/note="Vector: pCS107; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Average insert size 1.5 kb, range 0.5-4 kb. Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute). "
ORIGIN

Query Match 92.0%; Score 18.4; DB 4; Length 547;
Best Local Similarity 95.0%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        234 AAAGATGATTAGGCAGAGGT 253
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RESULT 2
BQ523985
LOCUS BQ523985 587 bp mRNA linear EST 10-JUN-2002
DEFINITION NISC_no02b04.x1 NICHD_XGC_Emb8 Xenopus tropicalis cDNA clone IMAGE:5379775 3', mRNA sequence.
ACCESSION BQ523985
VERSION BQ523985.1 GI:21382854
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 587)
AUTHORS NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
TITLE National Institute of Child Health and Human Development, National Cancer Insitute, Xenopus Gene Collection
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM11967 row: C column: 8
Seq primer: -21M13 forward primer (ABI).
FEATURES Location/Qualifiers
source 1. .587
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:5379775"
/tissue_type="tadpole"
/dev_stage="embryo, stages 40-45"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_Emb8"
/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 587;
Best Local Similarity 95.0%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        244 AAAGATGATTAGGCAGAGGT 263
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RESULT 3
CO359322
LOCUS CO359322 612 bp mRNA linear EST 29-JUN-2004
DEFINITION DR_ATE_SU03_G11 adult testis subtracted 1 (TLL) Danio rerio cDNA, mRNA sequence.
ACCESSION CO359322
VERSION CO359322.1 GI:49440639
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 612)
AUTHORS Li,Y., Chia,J.M., Bartfai,R., Christoffels,A., Yue,G.H., Ke,D., Ho,M.Y., Hill,J.A., Stupka,E. and Orban,L.
TITLE Comparative analysis of the testis and ovary transcriptomes in zebrafish by combining experimental and computational tools
JOURNAL Unpublished (2004)
COMMENT Contact: Laszlo ORBAN
Reproductive Genomics Group
Temasek Lifesciences Laboratory
1 Research Link, The NUS, Singapore 117 604
Tel: +65 6872 7413
Fax: +65 6872 7007
Email: laszlo@tll.org.sg

```
            Similar to Q9CUZ3
            High quality sequence stop: 612.
FEATURES              Location/Qualifiers
     source           1. .612
                      /organism="Danio rerio"
                      /mol_type="mRNA"
                      /strain="Toh (Singaporean strain)"
                      /db_xref="taxon:7955"
                      /sex="male"
                      /dev_stage="adult (fully mature)"
                      /clone_lib="adult testis subtracted 1 (TLL)"
                      /note="Organ: pooled testis; Vector: pT-Advantage; cDNA
                      was synthesized from adult testis and ovary total RNA
                      using SMART PCR cDNA synthesis kit (Clontech).
                      PCR-SelectTM cDNA subtraction kit (Clontech) was used to
                      enrich for fragments, which were present in the testis but
                      not in the ovary cDNA. The selectively amplified cDNA
                      fragments (in average 400-800bp in length) were ligated
                      into pT-Advantage (Clontech) and transformed into
                      XL10-Gold competent cells (Stratagene). The insert from
                      randomly selected white colonies was PCR amplified using
                      M13 forward and reverse primers and partially sequenced by
                      using M13 reverse primer."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 7;  Length 612;
  Best Local Similarity   95.0%;  Pred. No. 3.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||| ||||||||||||
Db        474 AGAGATGTTTAGGCAGAGGT 493


RESULT 4
CN090609
LOCUS       CN090609                689 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2BBA33CG11.b1 Xenopus tropicalis xtbs plasmid library Xenopus
            tropicalis cDNA clone xtbs33N21 3', mRNA sequence.
ACCESSION   CN090609
VERSION     CN090609.1  GI:45883305
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES              Location/Qualifiers
     source           1. .689
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /strain="ivory coast"
                      /db_xref="taxon:8364"
                      /clone="xtbs33N21"
                      /tissue_type="pool of brains and spinal cords from
                      tadpoles at stages 51-52 and 61-62"
                      /dev_stage="stage 51-52 and 61-62"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Xenopus tropicalis xtbs plasmid library"
                      /note="Vector: pCMVSPORT6_xtbs; Site_1: SfiI; Site_2:
                      SfiI; Xenopus tropicalis polyA+ RNA was obtained from
                      brain and spinal cord of tadpoles at stages 51-52 and
                      61-62. cDNAs were synthesized using the SMART system of
                      CLONTECH and directionally cloned into pCMVSPORT6_xtbs, a
                      modified version of pCMVSPORT6 allowing directional
                      cloning using asymetric SfiI sites. For antisense RNA
                      synthesis, use T7 promoter and for sense RNA use SP6
                      promoter. Library constructed by Dr. L. Coen and Prof. B.
                      Demeneix (Museum National d'Histoire Naturelle and CNRS
                      UMR 5166, Paris, France)."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 7;  Length 689;
  Best Local Similarity   95.0%;  Pred. No. 3.2e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        188 AAAGATGATTAGGCAGAGGT 207


RESULT 5
CN099540
LOCUS       CN099540                731 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2CAA16BD09.b1 Xenopus tropicalis xthr plasmid library Xenopus
            tropicalis cDNA clone xthr16G18 3', mRNA sequence.
ACCESSION   CN099540
VERSION     CN099540.1  GI:45892236
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES              Location/Qualifiers
     source           1. .731
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /strain="ivory coast"
                      /db_xref="taxon:8364"
                      /clone="xthr16G18"
                      /tissue_type="pool of heads and retinas from tailbud
                      stages 25-35"
                      /dev_stage="stage 25-35"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Xenopus tropicalis xthr plasmid library"
                      /note="Vector: pCMVSPORT6_xthr; Site_1: SfiI; Site_2:
                      SfiI; Xenopus tropicalis polyA+ RNA was obtained from pool
                      of heads and retinas from tailbud stages 25-35 cDNAs were
                      synthesized using the SMART system of CLONTECH and
                      directionally cloned into pCMVSPORT6_xthr, a modified
                      version of pCMVSPORT6 allowing directional cloning using
                      asymetric SfiI sites. For antisense RNA synthesis, use T7
                      promoter and for sense RNA use SP6 promoter. Library
                      constructed by Drs. N. Pollet, M. Perron, M. Wegnez, A.
                      Mazabraud (CNRS UMR 8080, Universite Paris Sud, Orsay,
                      France)."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 7;  Length 731;
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  Best Local Similarity   95.0%;  Pred. No. 3.2e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||||||||||||||||
Db        204 AAAGATGATTAGGCAGAGGT 223


RESULT 6
CO798651
LOCUS       CO798651                794 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  AGENCOURT_30340870 NIH_ZGC_14 Danio rerio cDNA clone IMAGE:7401252
            5', mRNA sequence.
ACCESSION   CO798651
VERSION     CO798651.1  GI:50986831
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 794)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: John Ngai, Nancy Freeman, NIDCD
             cDNA Library Preparation: Dr. Sumio Sugano
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15592  row: k  column: 10
            High quality sequence start: 4
            High quality sequence stop: 624.
FEATURES             Location/Qualifiers
     source          1. .794
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:7401252"
                     /tissue_type="olfactory epithelium"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_ZGC_14"
                     /note="Organ: olfactory epithelium; Vector: pME18S-FL3;
                     Site_1: DraIII; Site_2: DraIII; 1st strand cDNA was primed
                     with an oligo(dT) primer
                     [GCGGCTGAAGACGGCCTATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a DraIII adaptor
                     [GGCCUACUGG], digested and directionally cloned into
                     distinct DraIII sites of the pME18S-FL3. Library was size
                     selected for 1.0 kb, with a average insert size of ~1.2kb.
                     Library constructed by Yutaka Suzuki (University of Tokyo
                     Institute of Medical Science). Custom primers recommended
                     for sequencing: 5' end primer 5'-GGATGTTGCCTTTACTTCTA-3'
                     and 3' end primer 5'-CGACCTGCAGCTCGAGCACA-3'. Note: This
                     is a Zebrafish Gene Collection (ZGC) library"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 7;  Length 794;
  Best Local Similarity   95.0%;  Pred. No. 3.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||| ||||||||||||
Db        446 AGAGATGTTTAGGCAGAGGT 465


RESULT 7
BX693640
LOCUS       BX693640                859 bp    mRNA    linear   EST 14-NOV-2003
DEFINITION  BX693640 XGC-neurula Xenopus tropicalis cDNA clone TNeu087h08 3',
            mRNA sequence.
ACCESSION   BX693640
VERSION     BX693640.1  GI:38342760
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 859)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu087h08.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .859
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu087h08"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 5;  Length 859;
  Best Local Similarity   95.0%;  Pred. No. 3.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        247 AAAGATGATTAGGCAGAGGT 266


RESULT 8
CR417260
LOCUS       CR417260                869 bp    mRNA    linear   EST 13-JUN-2004
DEFINITION  CR417260 XGC-tailbud Xenopus tropicalis cDNA clone TTbA018g16 3',
            mRNA sequence.
ACCESSION   CR417260
VERSION     CR417260.1  GI:48685507
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 869)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
```

```
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: TTbA018g16.q1kT7
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: T7.
FEATURES              Location/Qualifiers
     source           1. .869
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TTbA018g16"
                      /dev_stage="tailbud (stage 28-30)"
                      /lab_host="Escherichia coli DH10B."
                      /clone_lib="XGC-tailbud"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                      was oligo dT primed from 5ug of poly A+ RNA from tailbud.
                      EcoRI-NotI cut cDNA was then ligated into pCS107 with
                      EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 7;  Length 869;
  Best Local Similarity   95.0%;  Pred. No. 3.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        254 AAAGATGATTAGGCAGAGGT 273


RESULT 9
CO812154
LOCUS       CO812154                886 bp    mRNA    linear   EST 06-AUG-2004
DEFINITION  AGENCOURT_30338237 NIH_ZGC_14 Danio rerio cDNA clone IMAGE:7402168
            5', mRNA sequence.
ACCESSION   CO812154
VERSION     CO812154.1  GI:51030780
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 886)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: John Ngai, Nancy Freeman, NIDCD
             cDNA Library Preparation: Dr. Sumio Sugano
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15595  row: a  column: 14
            High quality sequence stop: 695.
FEATURES              Location/Qualifiers
     source           1. .886
                      /organism="Danio rerio"
                      /mol_type="mRNA"
                      /db_xref="taxon:7955"
                      /clone="IMAGE:7402168"
                      /tissue_type="olfactory epithelium"
                      /lab_host="DH10B TonA"
                      /clone_lib="NIH_ZGC_14"
                      /note="Organ: olfactory epithelium; Vector: pME18S-FL3;
                      Site_1: DraIII; Site_2: DraIII; 1st strand cDNA was primed
                      with an oligo(dT) primer
                      [GCGGCTGAAGACGGCCTATGTGGCCTTTTTTTTTTTTTTTT];
                      double-stranded cDNA was ligated to a DraIII adaptor
                      [GGCCUACUGG], digested and directionally cloned into
                      distinct DraIII sites of the pME18S-FL3. Library was size
                      selected for 1.0 kb, with a average insert size of ~1.2kb.
                      Library constructed by Yutaka Suzuki (University of Tokyo
                      Institute of Medical Science). Custom primers recommended
                      for sequencing: 5' end primer 5'-GGATGTTGCCTTTACTTCTA-3'
                      and 3' end primer 5'-CGACCTGCAGCTCGAGCACA-3'. Note: This
                      is a Zebrafish Gene Collection (ZGC) library"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 7;  Length 886;
  Best Local Similarity   95.0%;  Pred. No. 3.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||| ||||||||||||
Db        453 AGAGATGTTTAGGCAGAGGT 472


RESULT 10
CR445414/c
LOCUS       CR445414                896 bp    mRNA    linear   EST 19-JUN-2004
DEFINITION  CR445414 XGC-tailbud Xenopus tropicalis cDNA clone TTbA012n19 5',
            mRNA sequence.
ACCESSION   CR445414
VERSION     CR445414.1  GI:48971001
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: TTbA012n19.p1kaSP6
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: SP6.
FEATURES              Location/Qualifiers
     source           1. .896
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TTbA012n19"
                      /dev_stage="tailbud (stage 28-30)"
                      /lab_host="Escherichia coli DH10B."
                      /clone_lib="XGC-tailbud"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                      was oligo dT primed from 5ug of poly A+ RNA from tailbud.
                      EcoRI-NotI cut cDNA was then ligated into pCS107 with
                      EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 7;  Length 896;
  Best Local Similarity   95.0%;  Pred. No. 3.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        841 AAAGATGATTAGGCAGAGGT 822
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RESULT 11
BX699062
LOCUS       BX699062                910 bp    mRNA    linear   EST 17-NOV-2003
DEFINITION  BX699062 XGC-neurula Xenopus tropicalis cDNA clone TNeu073a09 3',
            mRNA sequence.
ACCESSION   BX699062
VERSION     BX699062.1  GI:38361269
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu073a09.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu073a09"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 5;  Length 910;
  Best Local Similarity   95.0%;  Pred. No. 3.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        245 AAAGATGATTAGGCAGAGGT 264


RESULT 12
BX683124
LOCUS       BX683124                913 bp    mRNA    linear   EST 14-NOV-2003
DEFINITION  BX683124 XGC-neurula Xenopus tropicalis cDNA clone TNeu069h15, mRNA
            sequence.
ACCESSION   BX683124
VERSION     BX683124.1  GI:38332244
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu069h15.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu069h15"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 5;  Length 913;
  Best Local Similarity   95.0%;  Pred. No. 3.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        245 AAAGATGATTAGGCAGAGGT 264


RESULT 13
BX694706
LOCUS       BX694706                914 bp    mRNA    linear   EST 17-NOV-2003
DEFINITION  BX694706 XGC-neurula Xenopus tropicalis cDNA clone TNeu111c20 3',
            mRNA sequence.
ACCESSION   BX694706
VERSION     BX694706.1  GI:38343826
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu111c20.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
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                     /clone="TNeu111c20"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 5;  Length 914;
  Best Local Similarity   95.0%;  Pred. No. 3.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              | ||||||||||||||||||
Db        245 AAAGATGATTAGGCAGAGGT 264


RESULT 14
AW342249/c
LOCUS       AW342249                214 bp    mRNA    linear   EST 01-JAN-2001
DEFINITION  GthEST1 Guillardia theta Lambda Zap II cDNA Library Guillardia
            theta cDNA clone 38r, mRNA sequence.
ACCESSION   AW342249
VERSION     AW342249.1  GI:12000490
KEYWORDS    EST.
SOURCE      Guillardia theta
  ORGANISM  Guillardia theta
            Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
REFERENCE   1  (bases 1 to 214)
  AUTHORS   Fraunholz,M., Duebel,J., Wastl,J., Zauner,S. and Maier,U.-G.
  TITLE     EST Database of the cryptomonad alga: Guillardia theta
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Maier, U.-G.
            Department of Cell Biology and Applied Botany
            Philipps-University Marburg
            Karl-von-Frisch-Strasse, D-35043 Marburg, Germany
            Tel: ++49 6421 282 2057
            Fax: ++49 6421 282 1543
            Email: maier@mailer.uni-marburg.de.
FEATURES             Location/Qualifiers
     source          1. .214
                     /organism="Guillardia theta"
                     /mol_type="mRNA"
                     /strain="CCMP327"
                     /db_xref="taxon:55529"
                     /clone="38r"
                     /lab_host="SOLR"
                     /clone_lib="Guillardia theta Lambda Zap II cDNA Library"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 2;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GAGATGATTAGGCAGAGG 19
              ||||||||||||||||||
Db         78 GAGATGATTAGGCAGAGG 61


RESULT 15
AW215253/c
LOCUS       AW215253                354 bp    mRNA    linear   EST 06-DEC-1999
DEFINITION  up05g04.y1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:2651190 5'
            similar to TR:O00534 O00534 BREAST CANCER SUPPRESSOR CANDIDATE 1.
            ;, mRNA sequence.
ACCESSION   AW215253
VERSION     AW215253.1  GI:6525929
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            MGI:1031642
            Seq primer: -40RP from Gibco
            High quality sequence stop: 320.
FEATURES             Location/Qualifiers
     source          1. .354
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2651190"
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu30"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT-1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally.  Primer: Oligo
                     dT.   Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 2;  Length 354;
  Best Local Similarity   94.7%;  Pred. No. 9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGG 19
              | ||||||||||||||||||
Db         42 ATAGATGATTAGGCAGAGG 24


RESULT 16
BQ315666
LOCUS       BQ315666                494 bp    mRNA    linear   EST 17-MAY-2002
DEFINITION  CM3-CT0039-230799-001-a04 CT0039 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ315666
VERSION     BQ315666.1  GI:20921435
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 494)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
```

```
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-CT0039-
            230799-001-a04&t3=1999-07-23&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 139.
FEATURES              Location/Qualifiers
     source           1. .494
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /dev_stage="Adult"
                      /clone_lib="CT0039"
                      /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                      SmaI; A mini-library was made by cloning products derived
                      from  ORESTES PCR (U.S. Letters Patent application No.
                      196,716 -  Ludwig Institute for Cancer Research) profiles
                      into  the pUC 18 vector. Reverse transcription of tissue
                      mRNA and cDNA amplification were performed under low
                      stringency conditions."
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 5;  Length 494;
  Best Local Similarity   94.7%;  Pred. No. 9.4e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGG 19
              || |||||||||||||||||
Db        408 AGTGATGATTAGGCAGAGG 426


RESULT 17
BG440037/c
LOCUS       BG440037                680 bp    mRNA    linear   EST 15-MAR-2001
DEFINITION  GA__Ea0005K23f Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Ea0005K23f, mRNA sequence.
ACCESSION   BG440037
VERSION     BG440037.1  GI:13349687
KEYWORDS    EST.
SOURCE      Gossypium arboreum
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
            Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence stop: 600.
FEATURES              Location/Qualifiers
     source           1. .680
                      /organism="Gossypium arboreum"
                      /mol_type="mRNA"
                      /strain="AKA"
                      /cultivar="8400"
                      /db_xref="taxon:29729"
                      /clone="GA__Ea0005K23f"
                      /tissue_type="Fibers isolated from bolls harvested 7-10
                      dpa"
                      /lab_host="E. coli"
                      /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                      /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 4;  Length 680;
  Best Local Similarity   94.7%;  Pred. No. 9.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GAGATGATTAGGCAGAGGT 20
              |||||||||||||| |||||
Db        203 GAGATGATTAGGCGGAGGT 185


RESULT 18
BH039638
LOCUS       BH039638                741 bp    DNA     linear   GSS 17-JUL-2001
DEFINITION  RPCI-24-273E14.TJ RPCI-24 Mus musculus genomic clone
            RPCI-24-273E14, genomic survey sequence.
ACCESSION   BH039638
VERSION     BH039638.1  GI:14817784
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-24-273E14.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 273  row: E  column: 14
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .741
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-24-273E14"
                      /sex="Male"
                      /cell_type="Spleen/Brain"
                      /clone_lib="RPCI-24"
                      /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                      RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                      library was  cloned in the pTARBAC1 cloning vector at the
                      BamH1 sites using MboI  partially digested male C57BL/6J
                      DNA."
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 8;  Length 741;
  Best Local Similarity   94.7%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GAGATGATTAGGCAGAGGT 20
              ||||| |||||||||||||
Db        299 GAGATAATTAGGCAGAGGT 317
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RESULT 19
CNS029UK
LOCUS       CNS029UK                1032 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            249B13 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL187733
VERSION     AL187733.1  GI:7825837
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 1032)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1032
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="249B13"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG249CA07LP1~end : T7"
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 9;  Length 1032;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGG 19
              ||||||||| |||||||||
Db        387 AGAGATGATGAGGCAGAGG 405


RESULT 20
CNS027K3/c
LOCUS       CNS027K3                1044 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            243E11 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL184764
VERSION     AL184764.1  GI:7822868
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 1044)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1044
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="243E11"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG243AC06LP1~end : T7"
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 9;  Length 1044;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGG 19
              ||||||||| |||||||||
Db        396 AGAGATGATGAGGCAGAGG 378


RESULT 21
BB361792/c
LOCUS       BB361792                 248 bp    mRNA    linear   EST 12-JUL-2000
DEFINITION  BB361792 RIKEN full-length enriched, 16 days embryo head Mus
            musculus cDNA clone C130006N13 3' similar to X76772 M.musculus mRNA
            for ribosomal protein S3, mRNA sequence.
ACCESSION   BB361792
VERSION     BB361792.1  GI:9073620
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 248)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
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            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .248
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="C130006N13"
                     /sex="mixed"
                     /tissue_type="head"
                     /dev_stage="16 days embryo"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 16 days embryo
                     head"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 2;  Length 248;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AGATGATTAGGCAGAGG 19
              |||||||||||||||||
Db         74 AGATGATTAGGCAGAGG 58


RESULT 22
AQ355954/c
LOCUS       AQ355954                 490 bp    DNA     linear   GSS 24-JAN-1999
DEFINITION  CITBI-E1-2532A22.TR CITBI-E1 Homo sapiens genomic clone 2532A22,
            genomic survey sequence.
ACCESSION   AQ355954
VERSION     AQ355954.1  GI:4183127
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2532A22.TF
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2532A22"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 8;  Length 490;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GAGATGATTAGGCAGAG 18
              |||||||||||||||||
Db        462 GAGATGATTAGGCAGAG 446


RESULT 23
BF330446
LOCUS       BF330446                 145 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  MR2-BN0364-220800-012-b01 BN0364 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF330446
VERSION     BF330446.1  GI:11301194
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 145)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
```

```
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-BN0364-
            220800-012-b01&t3=2000-08-22&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 145.
FEATURES             Location/Qualifiers
     source          1. .145
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="BN0364"
                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 2;  Length 145;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||| |||| |||||||
Db         46 AGAGATGTTTAGTCAGAGGT 65


RESULT 24
BF330451
LOCUS       BF330451                146 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  MR2-BN0364-280800-010-b02 BN0364 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF330451
VERSION     BF330451.1  GI:11301199
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 146)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-BN0364-
            280800-010-b02&t3=2000-08-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 146.
FEATURES             Location/Qualifiers
     source          1. .146
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="BN0364"
                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 2;  Length 146;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||| |||| |||||||
Db         47 AGAGATGTTTAGTCAGAGGT 66


RESULT 25
BZ350602
LOCUS       BZ350602                387 bp    DNA     linear   GSS 12-NOV-2002
DEFINITION  ht58d07.g1 WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum
            bicolor genomic clone ht58d07 5', genomic survey sequence.
ACCESSION   BZ350602
VERSION     BZ350602.1  GI:24913429
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 387)
  AUTHORS   Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
            Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
            Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
  TITLE     Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: ht58  row: d  column: 07
            Seq primer: -21M13UnivRev
            Class: shotgun
            High quality sequence stop: 387.
FEATURES             Location/Qualifiers
     source          1. .387
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4558"
                     /clone="ht58d07"
                     /lab_host="JM107 or DH5a"
                     /clone_lib="WGS-SbicolorF (JM107 adapted methyl filtered)"
                     /note="Site_1: Xba I; Site_2: Xba I; The vector was
                     digested with XbaI and one nucleotide was added by fill in
                     in the recessive 3' end. The genomic DNA was nebulized,
                     end repaired, adaptor ligated and size fractionated using
                     sephadex. The resulting fragments were between 0.8 and 3
```

kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 387;
Best Local Similarity 90.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 AGAGATGATTAGGCAGAGGT 20
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Db        208 AGAGATGATTATTCAGAGGT 227
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RESULT 26
AJ713073
LOCUS AJ713073 388 bp mRNA linear EST 30-JUN-2004
DEFINITION AJ713073 LKPD01 Homo sapiens cDNA clone LKPD01049, mRNA sequence.
ACCESSION AJ713073
VERSION AJ713073.1 GI:49498685
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 388)
AUTHORS DePitta,C., Tombolan,L., Kronnie,G., Romualdi,C., Vitulo,N., Basso,G. and Lanfranchi,G.
TITLE A leukemia-enriched cDNA microarray platform identified new transcripts with relevance to the biology of leukemias
JOURNAL Unpublished (2004)
COMMENT Contact: DePitta C
Biology and CRIBI
University of Padova
Via U. Bassi, 58/B, 35131, ITALY.
FEATURES Location/Qualifiers
source 1. .388
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LKPD01049"
/tissue_type="bone marrow"
/clone_lib="LKPD01"
/note="caucasian"

ORIGIN

Query Match 84.0%; Score 16.8; DB 1; Length 388;
Best Local Similarity 90.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||| ||||| ||||||||||
Db         86 AGAAATGATGAGGCAGAGGT 105
```

RESULT 27
AA503497/c
LOCUS AA503497 407 bp mRNA linear EST 20-AUG-1997
DEFINITION nh59g10.s1 NCI_CGAP_Pr8 Homo sapiens cDNA clone IMAGE:956706 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA ;, mRNA sequence.
ACCESSION AA503497
VERSION AA503497.1 GI:2238464
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 407)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 538 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 330.
FEATURES Location/Qualifiers
source 1. .407
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:956706"
/sex="male"
/tissue_type="prostate"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr8"
/note="Vector: pAMP10; mRNA made from invasive prostate tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. "

ORIGIN

Query Match 84.0%; Score 16.8; DB 1; Length 407;
Best Local Similarity 90.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||| ||| ||||||||||
Db        351 AGAGAAGATGAGGCAGAGGT 332
```

RESULT 28
AJ572696
LOCUS AJ572696 423 bp mRNA linear EST 28-JUL-2003
DEFINITION AJ572696 HM3/RH2 Homo sapiens cDNA clone HSPD45782, mRNA sequence.
ACCESSION AJ572696
VERSION AJ572696.1 GI:33296557
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS Laveder,P., De Pitta,C., Vitulo,N., Valle,G. and Lanfranchi,G.
TITLE Oligo-directed RNase H cleavage of abundant mRNAs in skeletal muscle
JOURNAL Unpublished (2003)
COMMENT Contact: Laveder P
CRIBI Biotechnology Centre
University of Padua
Via U. Bassi 58/B, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at http://muscle.cribi.unipd.it
BIOLIMS code: sHr-000004-0-H07
Seq primer: PC2R.
FEATURES Location/Qualifiers
source 1. .423
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSPD45782"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/clone_lib="HM3/RH2"

ORIGIN

```
  Query Match            84.0%;  Score 16.8;  DB 1;  Length 423;
  Best Local Similarity  90.0%;  Pred. No. 1.8e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||| ||||| ||||||||||
Db         75 AGAAATGATGAGGCAGAGGT 94


RESULT 29
BX975154
LOCUS       BX975154                484 bp    DNA     linear   GSS 05-JUL-2004
DEFINITION  Reverse strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHPP76122, genomic survey sequence.
ACCESSION   BX975154
VERSION     BX975154.1  GI:49706577
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 484)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES             Location/Qualifiers
     source          1. .484
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHPP76122"
                     /clone_lib="MHPP"
ORIGIN

  Query Match            84.0%;  Score 16.8;  DB 9;  Length 484;
  Best Local Similarity  90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||||||||| ||| ||
Db        194 AGAGATGATTAGGAAGAAGT 213


RESULT 30
BE558110/c
LOCUS       BE558110                506 bp    mRNA    linear   EST 30-AUG-2000
DEFINITION  fl19f03.y1 Zebrafish Research Genetics C32 fin Danio rerio cDNA 5'
            similar to TR:O15249 O15249 PDZ DOMAIN PROTEIN. [2] TR:O60833
            ;contains element TAR1 repetitive element ;, mRNA sequence.
ACCESSION   BE558110
VERSION     BE558110.1  GI:9822600
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
            Research Genetics. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Research Genetics web
            address: http://www.researchgenetics.com/
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 470.
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /tissue_type="Fin"
                     /lab_host="GeneHogs (HS996, a phage-resistant isolate of
                     DH10B)"
                     /clone_lib="Zebrafish Research Genetics C32 fin"
                     /note="Vector: pT7T3D-Pac with a modified polylinker;
                     Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared
                     from zebrafish(C32) fin, and was then primed with a Not I
                     - oligo(dT) primer. Double-stranded cDNA was ligated to
                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is non-normalized. Library was
                     constructed by Ning Wu. NOTE: This clone is available
                     royalty-free through LLNL; contact the IMAGE Consortium
                     (info.llnl.gov)for further information"
ORIGIN

  Query Match            84.0%;  Score 16.8;  DB 2;  Length 506;
  Best Local Similarity  90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||| |||| ||||||||||
Db        385 AGAGGTGATCAGGCAGAGGT 366


RESULT 31
AZ336360
LOCUS       AZ336360                509 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0066A09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0066A09 R, genomic survey sequence.
ACCESSION   AZ336360
VERSION     AZ336360.1  GI:10405580
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0066  row: A  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 509.
FEATURES             Location/Qualifiers
     source          1. .509
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0066A09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 509;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||| |||||| |||
Db 68 AGAGATGATAAGGCAGGGGT 87

RESULT 32
AQ317545
LOCUS AQ317545 525 bp DNA linear GSS 04-MAY-1999
DEFINITION RPCI11-79I13.TJC RPCI-11 Homo sapiens genomic clone RPCI-11-79I13, genomic survey sequence.
ACCESSION AQ317545
VERSION AQ317545.1 GI:4048796
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 525)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: RPCI11-79I13.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .525
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7530156"
/db_xref="taxon:9606"
/clone="RPCI-11-79I13"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 525;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||| |||||| |||||||
Db 21 AGAGAGGATTAGACAGAGGT 40

RESULT 33
CB719936
LOCUS CB719936 526 bp mRNA linear EST 10-APR-2003
DEFINITION AMGNNUC:NRDG1-00073-C10-A nrdg1 (10855) Rattus norvegicus cDNA clone nrdg1-00073-c10 5', mRNA sequence.
ACCESSION CB719936
VERSION CB719936.1 GI:29777078
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 526)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00073 row: c column: 10.
FEATURES Location/Qualifiers
source 1. .526
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrdg1-00073-c10"
/tissue_type="Dorsal Root Ganglia"
/clone_lib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; rat dorsal root ganglia"

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 526;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||| ||||||||| ||||
Db 434 AGAGAAGATTAGGCAAAGGT 453

RESULT 34
BE605742
LOCUS BE605742 531 bp mRNA linear EST 30-AUG-2000
DEFINITION fl19f03.x1 Zebrafish Research Genetics C32 fin Danio rerio cDNA 3' similar to TR:O15249 O15249 PDZ DOMAIN PROTEIN. [2] TR:O60833 ;contains element TAR1 repetitive element ;, mRNA sequence.
ACCESSION BE605742
VERSION BE605742.1 GI:9863011
KEYWORDS EST.

```
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fl19f03.y1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
            Research Genetics. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Research Genetics web
            address: http://www.researchgenetics.com/
            Seq primer: T7 ET from Amersham
            High quality sequence stop: 426.
FEATURES             Location/Qualifiers
     source          1. .531
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /tissue_type="Fin"
                     /lab_host="GeneHogs (HS996, a phage-resistant isolate of
                     DH10B)"
                     /clone_lib="Zebrafish Research Genetics C32 fin"
                     /note="Vector: pT7T3D-Pac with a modified polylinker;
                     Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared
                     from zebrafish(C32) fin, and was then primed with a Not I
                     - oligo(dT) primer. Double-stranded cDNA was ligated to
                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is non-normalized. Library was
                     constructed by Ning Wu. NOTE: This clone is available
                     royalty-free through LLNL; contact the IMAGE Consortium
                     (info.llnl.gov)for further information"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 2;  Length 531;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||| |||| ||||||||||
Db        357 AGAGGTGATCAGGCAGAGGT 376


RESULT 35
BQ122423
LOCUS       BQ122423                533 bp    mRNA    linear   EST 17-APR-2002
DEFINITION  EST607999 GLSD Medicago truncatula cDNA clone pGLSD-28N20, mRNA
            sequence.
ACCESSION   BQ122423
VERSION     BQ122423.1  GI:20174385
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Grusak,M.A., Samac,D., Town,C.D., Van Aken,S., Utterback,T.,
            Cheung,F. and Fraser,C.M.
  TITLE     ESTs from late stage developing seeds of Medicago truncatula
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Grusak, M.A.
            USDA/ARS Children's Nutrition Research Center
            Baylor College of Medicine
            1100 Bates Street, Houston, TX 77030-2600, USA
            Tel: 713 798 7044
            Fax: 713 798 7078
            Email: mgrusak@bcm.tmc.edu
            TIGR sequence name: MTRAD82TK More information is available at:
            www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
FEATURES             Location/Qualifiers
     source          1. .533
                     /organism="Medicago truncatula"
                     /mol_type="mRNA"
                     /cultivar="A17"
                     /db_xref="taxon:3880"
                     /clone="pGLSD-28N20"
                     /tissue_type="Immature seeds"
                     /dev_stage="25 to 35 days after pollination"
                     /lab_host="XLOLR"
                     /clone_lib="GLSD"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Immature seeds, collected from pods ranging in age
                     from 25 to 35 days after pollination, were harvested from
                     greenhouse-grown plants. Seed were removed and separated
                     from pod walls and immediately frozen in liquid nitrogen.
                     Seeds throughout the age range were pooled for mRNA
                     extraction. cDNA was prepared from polyA+ enriched RNA.
                     The cDNA was directionally ligated into the Unizap XR
                     vector from Stratagene and packaged using Gigapack III
                     Gold packaging extracts. Plasmids containing cDNA inserts
                     were excised from the recombinant lambda-Zap phage using
                     Ex-assist helper phage and propagated in XLOLR cells."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 5;  Length 533;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||||||| |||||||| |
Db        384 AGAGATGATGAGGCAGAGTT 403


RESULT 36
CK766395
LOCUS       CK766395                537 bp    mRNA    linear   EST 24-FEB-2004
DEFINITION  eca01-43ms3-f11 Eca01 Eschscholzia californica cDNA clone
            eca01-43ms3-f11 5', mRNA sequence.
ACCESSION   CK766395
VERSION     CK766395.1  GI:42720294
KEYWORDS    EST.
SOURCE      Eschscholzia californica (California poppy)
  ORGANISM  Eschscholzia californica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
            Papaveraceae; Eschscholzioideae; Eschscholzia.
REFERENCE   1  (bases 1 to 537)
  AUTHORS   dePamphilis,C., Carlson,J., Ma,H., Tanksley,S., Field,D.,
            Leebens-Mack,J., Arrington,J., Zahn,L.M., Kong,H., Ilut,D.,
            Druckenmiller,M., Landherr,L., Hu,Y., Plock,S., Wall,K.,
            Chiorean,S., Albert,V., Doyle,J., Frohlich,M., Miller,W.,
            Oppenheimer,D., Soltis,D., Soltis,P. and Theissen,G.
  TITLE     Generation of ESTs from early flower buds of Eschscholzia
            californica
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Claude dePamphilis or James Leebens-Mack
            Mueller Laboratory
            Penn State University
            208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
```

State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions. Full sequence and original trace file are available from the Plant Genome Network website (http://pgn.cornell.edu)
Plate: eca01-43ms3 row: f column: 11
Seq primer: M13F.

FEATURES Location/Qualifiers
source 1. .537
/organism="Eschscholzia californica"
/mol_type="mRNA"
/cultivar="Aurantiaca Orange"
/db_xref="taxon:3467"
/clone="eca01-43ms3-f11"
/tissue_type="flower buds <= 2.5mm"
/dev_stage="millimeter buds"
/lab_host="SOLR"
/clone_lib="Eca01"
/note="Vector: pBluescript SK (+/-); Site_1: EcoRI; Site_2: XhoI; Plants were grown in greenhouse at Penn State from commercially available seeds. Only floral buds with diameter of 2.5 mm of less were collected. This is a directionally cloned, non-normalized library. Avg. insert length: 1702; Primers: M13F and M13R; Antibiotic: 50 ug/ml Ampicillin; Primary Titer: 7E6 pfu total; Amplified Titer: 1.68E11 pfu/ml; Mass Excised Titer: 5.6E8 total; This library has been generated by the Floral Genome Project (FGP). We would like to thank Huck Life Sciences Consortium for their assistance. The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115684). More information about the project can be obtained at http://fgp.bio.psu.edu"

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 537;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||| ||| ||||||
Db 337 AGAGATGATGAGGAAGAGGT 356

RESULT 37
AQ491131
LOCUS AQ491131 558 bp DNA linear GSS 24-APR-1999
DEFINITION RPCI-11-246M17.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-246M17, genomic survey sequence.
ACCESSION AQ491131
VERSION AQ491131.1 GI:4677005
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 558)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES Location/Qualifiers
source 1. .558
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7594384"
/db_xref="taxon:9606"
/clone="RPCI-11-246M17"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 558;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||||| ||| ||||||
Db 86 AGAGATGATGAGGCAGGGGT 105

RESULT 38
AQ554673
LOCUS AQ554673 568 bp DNA linear GSS 28-MAY-1999
DEFINITION RPCI-11-381N22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-381N22, genomic survey sequence.
ACCESSION AQ554673
VERSION AQ554673.1 GI:4913850
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 568)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: RPCI-11-381N22.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES Location/Qualifiers
source 1. .568
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7646253"
/db_xref="taxon:9606"
/clone="RPCI-11-381N22"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

RPCI11 Human Male BAC Library"
ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 568;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||| |||||| |||||||
Db 15 AGAGAGGATTAGTCAGAGGT 34

RESULT 39
BJ690447
LOCUS BJ690447 599 bp mRNA linear EST 23-APR-2004
DEFINITION BJ690447 HREST library Haplochromis sp. 'red tail sheller' cDNA clone no589h05, mRNA sequence.
ACCESSION BJ690447
VERSION BJ690447.1 GI:46533568
KEYWORDS EST.
SOURCE Haplochromis sp. 'red tail sheller'
ORGANISM Haplochromis sp. 'red tail sheller'
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei; Cichlidae; Haplochromis.
REFERENCE 1 (bases 1 to 599)
AUTHORS Watanabe,M., Kobayashi,N., Shin-i,T., Kohara,Y. and Okada,N.
TITLE Orf sequences of cichlid in Lake Victoria are essentially same
JOURNAL Unpublished (2004)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES Location/Qualifiers
source 1. .599
/organism="Haplochromis sp. 'red tail sheller'"
/mol_type="mRNA"
/db_xref="taxon:257976"
/clone="no589h05"
/tissue_type="jaw"
/dev_stage="varied"
/clone_lib="HREST library"
ORIGIN

Query Match 84.0%; Score 16.8; DB 4; Length 599;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||||| ||| ||||||||
Db 45 AGAGATGTTTAAGCAGAGGT 64

RESULT 40
CL186343/c
LOCUS CL186343 614 bp DNA linear GSS 06-JAN-2004
DEFINITION 104_401_10900146_116_32411_077 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10900146, genomic survey sequence.
ACCESSION CL186343
VERSION CL186343.1 GI:40698866
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 614)
AUTHORS Budiman,M.A., Flick,E., Jones,J., Nunberg,A., Citek,R.W., Robbins,D., Rohlfing,T., Bradford,K., Fries,J., McMenamy,J., Trani,L., Isak,A., Zimmerman,C., Lakey,N. and Bedell,J.A.
TITLE GeneThresher methylation filtered genomic sequences from Sorghum bicolor
JOURNAL Unpublished (2004)
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 401 row: c column: 18
Seq primer: T3 Reverse
Class: shotgun
High quality sequence stop: 614.
FEATURES Location/Qualifiers
source 1. .614
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="10900146"
/clone_lib="Sorghum methylation-filtered library (LibID: 104)"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 614;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAGATGATTAGGCAGAGGT 20
||||| ||||||| ||||||
Db 106 AGAGAGGATTAGGGAGAGGT 87

RESULT 41
B00642/c
LOCUS B00642 627 bp DNA linear GSS 13-JUL-1996
DEFINITION cSRL-117e7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-117e7, genomic survey sequence.
ACCESSION B00642
VERSION B00642.1 GI:1409920
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 627)
AUTHORS Evans,G.A., Burbee,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M., Jones,D., Ward,T., Gillilan,E., Schagemann,J., Probst,S. ., Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M., Kupfer,K. and Garner,H.R.
TITLE Genomic Sequence Sampled Map of Chromosome 11
JOURNAL Unpublished (1996)
COMMENT Contact: Evans GA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
Fax: 214-648-1666
Email: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu
PCR PRimers
FORWARD: CTCCTCATCTCTAACCTTCC
BACKWARD: GCATTGTGAGTTGGTTAGTC
Seq primer: T7
Class: cosmid ends
High quality sequence stop: 627.

```
FEATURES             Location/Qualifiers
     source          1. .627
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="cSRL-117e7"
                     /sex="female"
                     /cell_type="chimeric hamster somatic cell hybrid"
                     /clone_lib="cSRL flow sorted Chromosome 11 specific
                     cosmid"
                     /note="Vector: sCos-1; Human Chromosome 11 specific cosmid
                     library prepared from flow sorted human  Chromosome 11
                     derived from Chinese Hampster Ovary (CHO) monochromosomal
                     somatic cell hybrid, J1"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 8;  Length 627;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||||||  ||||||||||
Db         75 AGAGATGAGGAGGCAGAGGT 56


RESULT 42
CD304890
LOCUS       CD304890                663 bp    mRNA    linear   EST 16-SEP-2003
DEFINITION  StrPu691.001255 Sea urchin larva cDNA library MPMGp691
            Strongylocentrotus purpuratus cDNA clone
            MPMGp691C0520;MPI_SURUDI_20C5 5', mRNA sequence.
ACCESSION   CD304890
VERSION     CD304890.1  GI:34749939
KEYWORDS    EST.
SOURCE      Strongylocentrotus purpuratus
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A.,
            Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.
  TITLE     Generation, annotation, evolutionary analysis, and database
            integration of 20,000 unique sea urchin EST clusters
  JOURNAL   Genome Res. 13 (12), 2736-2746 (2003)
COMMENT     Contact: Poustka AJ
            laboraty 145, dept.Lehrach
            Max-Planck-Institut fuer Molekulare Genetik
            Ihnestr.63-73, D-14195 Berlin, Germany
            Tel: +49 30 8413 1235
            Fax: +49 30 8413 1128
            Email: poustka@molgen.mpg.de
            The library was characterised by oligonucleotide fingerprinting
            (ONF) to reduce sequencing redundancy. According to the ONF
            procedure, clones that display the same hybridisation matrix with a
            battery of 200 8mer oligonucleotides are grouped into clusters. One
            clone per ONF cluster is selected for sequencing. The size of each
            cluster is an indicator of the frequency of a transcript in the
            analysed library. The cluster size as well as the coordinates of
            the other clones assigned to the same ONF cluster as the clone from
            which the above EST is generated is available at the sea urchin
            project web site at: http://www.molgen.mpg.de/ag_seaurchin/ . cDNA
            clones and filters are distributed via the Resource Center/Primary
            Database of the German Human Genome Project (http://www.rzpd.de)
            PCR PRimers
            FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq
            BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-seq
            Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Strongylocentrotus purpuratus"
                     /mol_type="mRNA"
                     /db_xref="taxon:7668"
                     /clone="MPMGp691C0520;MPI_SURUDI_20C5"
                     /tissue_type="whole larva"
                     /dev_stage="larva 2-3 weeks"
                     /lab_host="E.coli, XL1 blue"
                     /clone_lib="Sea urchin larva cDNA library MPMGp691"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI; Random
                     primed and directionally cloned in pSport1 vector using a
                     NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC (T)15-3' and a
                     SalI 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 6;  Length 663;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||| ||||||| ||||||
Db        133 AGAGAAGATTAGGAAGAGGT 152


RESULT 43
BH975438
LOCUS       BH975438                699 bp    DNA     linear   GSS 02-OCT-2002
DEFINITION  odh59a02.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BH975438
VERSION     BH975438.1  GI:23458441
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 699)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: odh59  row: a  column: 02
            Seq primer: -28RPpOT reverse
            Class: shotgun
            High quality sequence start: 49
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .699
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="B.oleracea002"
                     /note="Vector: pOTw13; Whole genome shotgun library from
                     flowering buds. DNA was purified  from a crude nuclear
                     prep using Brassica oleracea TO1000DH3 buds  provided by
                     Thosmas Osborn at the University of Wisconsin. Genomic
                     DNA was provided by Pablo Rabinowicz (CSHL) and the
                     shotgun library  prepared at Washington University Genome
                     Sequencing Center."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 8;  Length 699;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||| |||||| ||||||||
Db        103 AGAGGTGATTAAGCAGAGGT 122


RESULT 44
```

```
BH973998/c
LOCUS       BH973998                707 bp    DNA     linear   GSS 02-OCT-2002
DEFINITION  odh10c03.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BH973998
VERSION     BH973998.1  GI:23457001
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 707)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: odh10  row: c  column: 03
            Seq primer: -21UPpOT forward
            Class: shotgun
            High quality sequence start: 16
            High quality sequence stop: 551.
FEATURES             Location/Qualifiers
     source          1. .707
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="B.oleracea002"
                     /note="Vector: pOTw13; Whole genome shotgun library from
                     flowering buds. DNA was purified  from a crude nuclear
                     prep using Brassica oleracea TO1000DH3 buds  provided by
                     Thosmas Osborn at the University of Wisconsin. Genomic
                     DNA was provided by Pablo Rabinowicz (CSHL) and the
                     shotgun library  prepared at Washington University Genome
                     Sequencing Center."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 8;  Length 707;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              || |||||||| ||||||||
Db        575 AGGGATGATTAAGCAGAGGT 556


RESULT 45
CN791475/c
LOCUS       CN791475                716 bp    mRNA    linear   EST 26-MAY-2004
DEFINITION  4126207 BARC 8BOV Bos taurus cDNA clone 8BOV_42M11 5', mRNA
            sequence.
ACCESSION   CN791475
VERSION     CN791475.1  GI:47687455
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 716)
  AUTHORS   Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
            Matukumalli,L.K.
  TITLE     Construction and Analysis of a cDNA Library Generated From
            Intestinal Muscle and Epithelial Tissues of Holstein Cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Richard G. Baumann
            Bovine Functional Genomics Lab
            ANRI
            BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
            Tel: 3015048604
            Fax: 3015048744
            Email: rbaumann@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt '' -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 18
            Plate: 42  row: M  column: 11
            Seq primer: CCTATTTAGGTGACACTATAGAAC
            High quality sequence stop: 716.
FEATURES             Location/Qualifiers
     source          1. .716
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="8BOV_42M11"
                     /sex="Female"
                     /tissue_type="Epithelial, Muscle"
                     /dev_stage="Lactating, Neonatal"
                     /lab_host="DH10B TonA"
                     /clone_lib="BARC 8BOV"
                     /note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
                     NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
                     library in pCMVsport6.1, constructed from equimolar mRNA
                     pools derived from 5 sources, 4 lactating intestinal, 1
                     neonatal intestinal 4/5 Lactating, Proximal Duodenum,
                     Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
                     Duodenum, Jejunum, Distal Ileum"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 7;  Length 716;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||| ||| ||||||||||||
Db        258 AGACATGCTTAGGCAGAGGT 239


RESULT 46
AZ519049
LOCUS       AZ519049                718 bp    DNA     linear   GSS 16-OCT-2000
DEFINITION  RPCI-11-79I13.TJD RPCI-11 Homo sapiens genomic clone RPCI-11-79I13,
            genomic survey sequence.
ACCESSION   AZ519049
VERSION     AZ519049.1  GI:10830166
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 718)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     BAC end sequences of library RPCI-11
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI11-79I13.TJC RPCI11-79I13.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            This BAC end was generated during the R&D process and may have
            higher chance of clone tracking errors.
            Seq primer: SP6
```

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          Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .718
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="GDB:7530156"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-79I13"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /clone_lib="RPCI-11"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 8;  Length 718;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||| |||||| |||||||
Db         32 AGAGAGGATTAGACAGAGGT 51


RESULT 47
BQ782214/c
LOCUS       BQ782214                729 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  UI-R-FF0-cpj-o-14-0-UI.s1 NCI_CGAP_FF0 Rattus norvegicus cDNA clone
            UI-R-FF0-cpj-o-14-0-UI 3', mRNA sequence.
ACCESSION   BQ782214
VERSION     BQ782214.1  GI:21990686
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 729)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Jeff Stevens
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: DISTRIBUTION: Researchers may obtain clones
            from Research Genetics (www.resgen.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="UI-R-FF0-cpj-o-14-0-UI"
                     /tissue_type="Mixed tissues"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="NCI_CGAP_FF0"
                     /note="Vector: pT7T3-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoR I; Site_2: Not I; UI-R-FF0 is a
                     subtracted cDNA library containing the following
                     tissue(s): Normal cartilage and SR-JWS Tumor Line . The
                     subtraction was made according to Bonaldo, Lennon and
                     Soares, Genome Research, 6:791-806, 1996. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for these libraries are: CTAATGGACG,
                     CATTCTTGTA.
                     TAG_TISSUE=rat SRC-JWST tumor line
                     TAG_LIB=UI-R-FF0
                     TAG_SEQ=CATTCTTGTA"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 5;  Length 729;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              ||||| |||||||||| ||||
Db        585 AGAGAAGATTAGGCAAAGGT 566


RESULT 48
CL189821/c
LOCUS       CL189821                734 bp    DNA     linear   GSS 06-JAN-2004
DEFINITION  104_407_10905649_114_32475_007 Sorghum methylation-filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10905649, genomic survey
            sequence.
ACCESSION   CL189821
VERSION     CL189821.1  GI:40702344
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 734)
  AUTHORS   Budiman,M.A., Flick,E., Jones,J., Nunberg,A., Citek,R.W.,
            Robbins,D., Rohlfing,T., Bradford,K., Fries,J., McMenamy,J.,
            Trani,L., Isak,A., Zimmerman,C., Lakey,N. and Bedell,J.A.
  TITLE     GeneThresher methylation filtered genomic sequences from Sorghum
            bicolor
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 407  row: i  column: 01
            Seq primer: M13/pUC Forward
            Class: shotgun
            High quality sequence stop: 734.
FEATURES             Location/Qualifiers
     source          1. .734
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10905649"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 9;  Length 734;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||||||||| |||| ||
Db        159 AGAGATGATTAGACAGATGT 140


RESULT 49
BZ345634
LOCUS       BZ345634                746 bp    DNA     linear   GSS 12-NOV-2002
DEFINITION  hs87c01.b1 WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum
            bicolor genomic clone hs87c01 5', genomic survey sequence.
ACCESSION   BZ345634
VERSION     BZ345634.1  GI:24903898
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
            Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
            Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
  TITLE     Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: hs87  row: c  column: 01
            Seq primer: -21M13UnivFwd
            Class: shotgun
            High quality sequence stop: 746.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4558"
                     /clone="hs87c01"
                     /lab_host="JM107 or DH5a"
                     /clone_lib="WGS-SbicolorF (JM107 adapted methyl filtered)"
                     /note="Site_1: Xba I; Site_2: Xba I; The vector was
                     digested with XbaI and one nucleotide was added by fill in
                     in the recessive 3' end. The genomic DNA was nebulized,
                     end repaired, adaptor ligated and size fractionated using
                     sephadex. The resulting fragments were between 0.8 and 3
                     kb and were cloned into the vector (.x/y reads in M13mp19,
                     .b/g reads in pUC19). The same ligation was transformed in
                     either JM107 or DH5a."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 8;  Length 746;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||||||||  |||||||
Db        409 AGAGATGATTATTCAGAGGT 428


RESULT 50
CR100681/c
LOCUS       CR100681                753 bp    DNA     linear   GSS 05-JUL-2004
DEFINITION  Forward strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHPP113b19, genomic survey sequence.
ACCESSION   CR100681
VERSION     CR100681.1  GI:49848081
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES             Location/Qualifiers
     source          1. .753
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHPP113b19"
                     /clone_lib="MHPP"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 9;  Length 753;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAGATGATTAGGCAGAGGT 20
              |||||||||| || |||||||
Db         75 AGAGATGATTGGGGAGAGGT 56


Search completed: December 15, 2004, 16:49:26
Job time : 1350.5 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 15, 2004, 09:10:16 ; Search time 764 Seconds
(without alignments)
1237.950 Million cell updates/sec

Title: US-08-901-612A-58
Perfect score: 20
Sequence: 1 agagaugauuaggcagaggt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	AR027809	AR027809 Sequence
2	c	20	100.0	27	6	AX147024	AX147024 Sequence
3		20	100.0	30	6	AR027810	AR027810 Sequence
4		20	100.0	30	6	AR027840	AR027840 Sequence
5	c	20	100.0	87	6	AX151115	AX151115 Sequence
6	c	20	100.0	93	14	HPBPRECAA	D30625 Hepatitis B
7	c	20	100.0	99	14	HPBPRECA	M76687 Hepatitis B
8	c	20	100.0	99	14	HPBPRECB	M76688 Hepatitis B
9	c	20	100.0	99	14	HPBPRECC	M76689 Hepatitis B
10	c	20	100.0	99	14	HPBPRECD	M76690 Hepatitis B
11	c	20	100.0	99	14	HPBPRECE	M76691 Hepatitis B
12	c	20	100.0	99	14	HPBPRECF	M76692 Hepatitis B
13	c	20	100.0	99	14	HPBPRECG	M76693 Hepatitis B
14	c	20	100.0	99	14	HPBPRECH	M76694 Hepatitis B
15	c	20	100.0	99	14	HPBPRECI	M76695 Hepatitis B
16	c	20	100.0	99	14	HPBPRECK	M76697 Hepatitis B
17	c	20	100.0	99	14	HPBPRECL	M76698 Hepatitis B
18	c	20	100.0	99	14	HPBPRECM	M76699 Hepatitis B
19	c	20	100.0	129	6	AX151114	AX151114 Sequence
20	c	20	100.0	150	14	AF528205	AF528205 Hepatitis
21	c	20	100.0	150	14	AF528206	AF528206 Hepatitis
22	c	20	100.0	150	14	AF528207	AF528207 Hepatitis
23	c	20	100.0	150	14	AF528208	AF528208 Hepatitis
24	c	20	100.0	150	14	AF528209	AF528209 Hepatitis
25	c	20	100.0	150	14	AF528210	AF528210 Hepatitis
26	c	20	100.0	150	14	AF528211	AF528211 Hepatitis
27	c	20	100.0	150	14	AF528212	AF528212 Hepatitis
28	c	20	100.0	150	14	AF528213	AF528213 Hepatitis
29	c	20	100.0	150	14	AF528214	AF528214 Hepatitis
30	c	20	100.0	150	14	AF528215	AF528215 Hepatitis
31	c	20	100.0	150	14	AF528216	AF528216 Hepatitis
32	c	20	100.0	150	14	AF528217	AF528217 Hepatitis
33	c	20	100.0	150	14	AF528218	AF528218 Hepatitis
34	c	20	100.0	150	14	AF528219	AF528219 Hepatitis
35	c	20	100.0	150	14	AF528220	AF528220 Hepatitis
36	c	20	100.0	150	14	AF528221	AF528221 Hepatitis
37	c	20	100.0	150	14	AF528222	AF528222 Hepatitis
38	c	20	100.0	150	14	AF528224	AF528224 Hepatitis
39	c	20	100.0	150	14	AF528225	AF528225 Hepatitis
40	c	20	100.0	150	14	AF528226	AF528226 Hepatitis
41	c	20	100.0	150	14	AF528227	AF528227 Hepatitis
42	c	20	100.0	150	14	AF528228	AF528228 Hepatitis
43	c	20	100.0	150	14	AF528229	AF528229 Hepatitis
44	c	20	100.0	150	14	AF528231	AF528231 Hepatitis
45	c	20	100.0	150	14	AF528232	AF528232 Hepatitis
46	c	20	100.0	150	14	AF528233	AF528233 Hepatitis
47	c	20	100.0	150	14	AF528234	AF528234 Hepatitis
48	c	20	100.0	150	14	AF528235	AF528235 Hepatitis
49	c	20	100.0	150	14	AF528236	AF528236 Hepatitis
50	c	20	100.0	150	14	AF528237	AF528237 Hepatitis
51	c	20	100.0	150	14	AF528238	AF528238 Hepatitis
52	c	20	100.0	150	14	AF528239	AF528239 Hepatitis
53	c	20	100.0	150	14	AF528240	AF528240 Hepatitis
54	c	20	100.0	150	14	AF528241	AF528241 Hepatitis
55	c	20	100.0	150	14	AF528242	AF528242 Hepatitis
56	c	20	100.0	150	14	AF528243	AF528243 Hepatitis
57	c	20	100.0	150	14	AF528244	AF528244 Hepatitis
58	c	20	100.0	150	14	AF528245	AF528245 Hepatitis
59	c	20	100.0	150	14	AF528246	AF528246 Hepatitis
60	c	20	100.0	150	14	AF528247	AF528247 Hepatitis
61	c	20	100.0	150	14	AF528248	AF528248 Hepatitis
62	c	20	100.0	150	14	AF528249	AF528249 Hepatitis
63	c	20	100.0	150	14	AF528250	AF528250 Hepatitis
64	c	20	100.0	150	14	AF528251	AF528251 Hepatitis
65	c	20	100.0	150	14	AF528252	AF528252 Hepatitis
66	c	20	100.0	150	14	AF528253	AF528253 Hepatitis
67	c	20	100.0	150	14	AF528254	AF528254 Hepatitis
68	c	20	100.0	150	14	AF528255	AF528255 Hepatitis
69	c	20	100.0	150	14	AF528256	AF528256 Hepatitis
70	c	20	100.0	150	14	AF528257	AF528257 Hepatitis
71	c	20	100.0	150	14	AF528258	AF528258 Hepatitis
72	c	20	100.0	150	14	AF528259	AF528259 Hepatitis
73	c	20	100.0	150	14	AF528261	AF528261 Hepatitis
74	c	20	100.0	150	14	AF528263	AF528263 Hepatitis
75	c	20	100.0	150	14	AF528264	AF528264 Hepatitis
76	c	20	100.0	150	14	AF528265	AF528265 Hepatitis
77	c	20	100.0	150	14	AF528266	AF528266 Hepatitis
78	c	20	100.0	150	14	AF528267	AF528267 Hepatitis
79	c	20	100.0	150	14	AF528268	AF528268 Hepatitis
80	c	20	100.0	150	14	AF528269	AF528269 Hepatitis
81	c	20	100.0	150	14	AF528270	AF528270 Hepatitis
82	c	20	100.0	150	14	AF528271	AF528271 Hepatitis
83	c	20	100.0	150	14	AF528272	AF528272 Hepatitis
84	c	20	100.0	150	14	AF528273	AF528273 Hepatitis
85	c	20	100.0	150	14	AF528274	AF528274 Hepatitis
86	c	20	100.0	150	14	AF528275	AF528275 Hepatitis
87	c	20	100.0	150	14	AF528276	AF528276 Hepatitis
88	c	20	100.0	150	14	AF528277	AF528277 Hepatitis
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91	c	20	100.0	150	14	AF528280	AF528280 Hepatitis
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c 93	20	100.0	150	14	AF528282	AF528282 Hepatitis
c 94	20	100.0	150	14	AF528283	AF528283 Hepatitis
c 95	20	100.0	150	14	AF528284	AF528284 Hepatitis
c 96	20	100.0	150	14	AF528286	AF528286 Hepatitis
c 97	20	100.0	150	14	AF528287	AF528287 Hepatitis
c 98	20	100.0	150	14	AF528288	AF528288 Hepatitis
c 99	20	100.0	150	14	AF528289	AF528289 Hepatitis
c 100	20	100.0	150	14	AF528290	AF528290 Hepatitis

ALIGNMENTS

```
RESULT 1
AR027809
LOCUS       AR027809                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 7 from patent US 5856459.
ACCESSION   AR027809
VERSION     AR027809.1  GI:5938629
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Frank,B.L., Roberts,P.C., Goodchild,J., Craig,J.Charles. and
            Mills,J.S.
  TITLE     Oligonucleotides specific for hepatitis B virus
  JOURNAL   Patent: US 5856459-A 7 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 17;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db          1 AGAGATGATTAGGCAGAGGT 20


RESULT 2
AX147024/c
LOCUS       AX147024                 27 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 18 from Patent WO0137291.
ACCESSION   AX147024
VERSION     AX147024.1  GI:14346295
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weindel,K., Riedling,M. and Geiger,A.
  TITLE     Magnetic glass particles, method for their preparation and uses
            thereof
  JOURNAL   Patent: WO 0137291-A 18 25-MAY-2001;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide primer (HBV reverse)"
     modified_base   27
                     /note="derivatization with a p-(t-butyl)benzyl-residue"
                     /mod_base=OTHER
ORIGIN

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Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         21 AGAGATGATTAGGCAGAGGT 2


RESULT 3
AR027810
LOCUS       AR027810                 30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5856459.
ACCESSION   AR027810
VERSION     AR027810.1  GI:5938630
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Frank,B.L., Roberts,P.C., Goodchild,J., Craig,J.Charles. and
            Mills,J.S.
  TITLE     Oligonucleotides specific for hepatitis B virus
  JOURNAL   Patent: US 5856459-A 8 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 30;
  Best Local Similarity   85.0%;  Pred. No. 17;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         11 AGAGATGATTAGGCAGAGGT 30


RESULT 4
AR027840
LOCUS       AR027840                 30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 38 from patent US 5856459.
ACCESSION   AR027840
VERSION     AR027840.1  GI:5938660
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Frank,B.L., Roberts,P.C., Goodchild,J., Craig,J.Charles. and
            Mills,J.S.
  TITLE     Oligonucleotides specific for hepatitis B virus
  JOURNAL   Patent: US 5856459-A 38 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 30;
  Best Local Similarity   85.0%;  Pred. No. 17;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db          1 AGAGATGATTAGGCAGAGGT 20


RESULT 5
AX151115/c
LOCUS       AX151115                 87 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0138498.
ACCESSION   AX151115
VERSION     AX151115.1  GI:14533317
KEYWORDS    .
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```
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stuyver,L., Schinazi,R., de Gendt,S., van Geyt,C., Zoulim,F.,
            Fried,M. and Rossau,R.
  TITLE     A new genotype of hepatitis b virus
  JOURNAL   Patent: WO 0138498-A 4 31-MAY-2001;
            Pharmasset, Inc. (US) ; INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .87
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 87;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 6
HPBPRECAA/c
LOCUS       HPBPRECAA                  93 bp    DNA     linear   VRL 24-JAN-2003
DEFINITION  Hepatitis B virus variant B3 genomic RNA, entire pre-C region.
ACCESSION   D30625 D01192
VERSION     D30625.1  GI:484048
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Galibert,F., Mandart,E., Fitoussi,F., Tiollais,P. and Charnay,P.
  TITLE     Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
            cloned in E. coli
  JOURNAL   Nature 281 (5733), 646-650 (1979)
  MEDLINE   81012091
   PUBMED   399327
REFERENCE   2  (bases 1 to 93)
  AUTHORS   Li,J., Tong,S., Vitvitski,L., Zoulim,F. and Trepo,C.
  TITLE     Rapid detection and further characterization of infection with
            hepatitis B virus variants containing a stop codon in the distal
            pre-C region
  JOURNAL   J. Gen. Virol. 71 (Pt 9), 1993-1998 (1990)
  MEDLINE   91011344
   PUBMED   2212990
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
                     /note="HBeAg-negative HBV variant B3~pre-C region"
     gene            1. .93
                     /gene="pre-C/C"
     CDS             1. .>93
                     /gene="pre-C/C"
                     /codon_start=1
                     /product="pre-C/C protein"
                     /protein_id="BAA06312.1"
                     /db_xref="GI:507810"
                     /translation="MQLFHLCLIISCTCPTFQASKLCLGWLWGMD"
     variation       25
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="aa or ac"
     variation       37
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="t"
     variation       42
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="c"
     variation       45
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="t"
     variation       49
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="g"
     variation       75
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2 and WO(wild-type)"
                     /replace="g"
     variation       87
                     /gene="pre-C/C"
                     /note="Base substitution has occurred at this position in
                     E2"
                     /replace="cc"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 93;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 7
HPBPRECA/c
LOCUS       HPBPRECA                   99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type1 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76687
VERSION     M76687.1  GI:485341
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45507.1"
                     /db_xref="GI:485342"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
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     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 1 (creates internal stop
                     codon)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 8
HPBPRECB/c
LOCUS       HPBPRECB                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 2precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76688
VERSION     M76688.1  GI:485343
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     variation       2
                     /note="c in wt; t in virus type 2"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45508.1"
                     /db_xref="GI:485344"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 2 (creates internal stop
                     codon)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 9
HPBPRECC/c
LOCUS       HPBPRECC                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 3precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76689
VERSION     M76689.1  GI:485345
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     variation       6
                     /note="c in wt; t in virus type 3"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45509.1"
                     /db_xref="GI:485346"
                     /translation="MQLFHLCLIISCSCPTFQASKLCLGWL"
     variation       58
                     /gene="C"
                     /note="g in wt; t in virus type 3 (val to phe)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 3 (creates internal stop
                     codon)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 10
HPBPRECD/c
LOCUS       HPBPRECD                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 4 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76690
VERSION     M76690.1  GI:485347
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45510.1"
                     /db_xref="GI:485348"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 4 (creates internal stop
                     codon)"
     variation       95
                     /note="g in wt; a in virus type 4 (gly to asp)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 11
HPBPRECE/c
LOCUS       HPBPRECE                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 5 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76691
VERSION     M76691.1  GI:485349
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     CDS             10. .93
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45511.1"
                     /db_xref="GI:485350"
                     /translation="MQLFHLCLIISCSCPTVQPSKLCLGWL"
     variation       64. .67
                     /gene="C"
                     /note="gcc in wt; ccg in virus type 5 (ala to pro)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 5 (creates internal stop
                     codon)"
     variation       95
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 12
HPBPRECF/c
LOCUS       HPBPRECF                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 6 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76692
VERSION     M76692.1  GI:485351
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .99
                     /gene="C"
     misc_feature    10. .99
                     /gene="C"
                     /product="precore protein"
                     /note="putative cds"
     variation       11
                     /gene="C"
                     /note="t in wt; c in virus type 6 (loss of start codon)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 13
HPBPRECG/c
LOCUS       HPBPRECG                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 7 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76693
VERSION     M76693.1  GI:485352
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
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COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     misc_feature    10. .93
                     /gene="C"
                     /product="precore protein"
                     /standard_name="pre-C region note: putative CDS"
     variation       10
                     /gene="C"
                     /note="a in wt; t in virus type 7 (loss of start codon)"
     variation       14
                     /gene="C"
                     /note="a in wt; g in virus type 7 (gln to arg)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 7 ( creates internal stop
                     codon)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 14
HPBPRECH/c
LOCUS       HPBPRECH                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 8 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76694
VERSION     M76694.1  GI:485353
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     misc_feature    10. .93
                     /gene="C"
                     /product="precore protein"
                     /standard_name="pre-C region note: putative CDS"
     variation       12
                     /gene="C"
                     /note="g in wt; t in virus type 8 (loss of start codon)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 8 (creates internal stop
                     codon)"
     variation       95
                     /note="g in wt; a in virus type 8 (gly to asp)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 15
HPBPRECI/c
LOCUS       HPBPRECI                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 9 precore protein (pre-C region, C) gene, 5'
            end.
ACCESSION   M76695
VERSION     M76695.1  GI:485354
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .93
                     /gene="C"
     misc_feature    10. .93
                     /gene="C"
                     /product="precore protein"
                     /standard_name="pre-C region note: putative CDS"
     variation       13
                     /gene="C"
                     /note="c in wt; t in virus type 9 (creates internal stop
                     codon)"
     variation       92
                     /gene="C"
                     /note="g in wt; a in virus type 9 (creates internal stop
                     codon)"
     variation       95
                     /note="g in wt; a in virus type 9 (gly to asp)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 16
HPBPRECK/c
LOCUS       HPBPRECK                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 11 precore protein (pre-C region, C) gene,
            5' end.
ACCESSION   M76697
VERSION     M76697.1  GI:485357
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
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           Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE  1  (bases 1 to 99)
  AUTHORS  Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
           Will,H.
  TITLE    Prevalence and type of pre-C HBV mutants in anti-HBe positive
           carriers with chronic liver disease in a highly endemic area
  JOURNAL  Virology 183 (2), 840-844 (1991)
  MEDLINE  91306476
   PUBMED  1853582
COMMENT    Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .99
                     /gene="C"
     CDS             10. .>99
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45513.1"
                     /db_xref="GI:485358"
                     /translation="MQLFHLCLIISVHVLLFKPPSCALGGPGTW"
     variation       42. .43
                     /gene="C"
                     /note="frameshift mutation, deletion of single base in
                     virus type 11"
     variation       94
                     /gene="C"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 17
HPBPRECL/c
LOCUS       HPBPRECL                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 12 precore protein (pre-C region, C) gene,
            5' end.
ACCESSION   M76698
VERSION     M76698.1  GI:485359
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .99
                     /gene="C"
     CDS             10. .>99
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45514.1"
                     /db_xref="GI:485360"
                     /translation="MQLFHLCLIISVHVLLFKPPSCALGGFRTW"
     variation       41. .42
                     /gene="C"
                     /note="frameshift mutation, deletion of single base in
                     virus type 12"
     variation       90
                     /gene="C"
                     /note="t in wt position 91; a in virus type 12 position
                     90"
     variation       93
                     /gene="C"
                     /note="g in wt position 94; a in virus type 12 position
                     93"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 18
HPBPRECM/c
LOCUS       HPBPRECM                  99 bp    DNA     linear   VRL 11-MAY-1994
DEFINITION  Hepatitis B virus type 13 precore protein (pre-C region, C) gene,
            5' end.
ACCESSION   M76699
VERSION     M76699.1  GI:485361
KEYWORDS    e antigen; precore protein; tolerogen.
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
            Will,H.
  TITLE     Prevalence and type of pre-C HBV mutants in anti-HBe positive
            carriers with chronic liver disease in a highly endemic area
  JOURNAL   Virology 183 (2), 840-844 (1991)
  MEDLINE   91306476
   PUBMED   1853582
COMMENT     Original source text: Hepatitis B virus DNA.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
     gene            10. .99
                     /gene="C"
     CDS             10. .>99
                     /gene="C"
                     /standard_name="pre-C region"
                     /codon_start=1
                     /product="precore protein"
                     /protein_id="AAA45515.1"
                     /db_xref="GI:485362"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWDM"
     variation       95
                     /gene="C"
                     /note="g in wt; a in virus type 13 (gly to asp)"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 99;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
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Db         42 AGAGATGATTAGGCAGAGGT 23


RESULT 19
AX151114/c
LOCUS       AX151114                129 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3 from Patent WO0138498.
ACCESSION   AX151114
VERSION     AX151114.1  GI:14533316
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stuyver,L., Schinazi,R., de Gendt,S., van Geyt,C., Zoulim,F.,
            Fried,M. and Rossau,R.
  TITLE     A new genotype of hepatitis b virus
  JOURNAL   Patent: WO 0138498-A 3 31-MAY-2001;
            Pharmasset, Inc. (US) ; INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .129
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 129;
  Best Local Similarity   85.0%;  Pred. No. 16;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 20
AF528205/c
LOCUS       AF528205                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1123 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528205
VERSION     AF528205.1  GI:32810971
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1123"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87556.1"
                     /db_xref="GI:32810972"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLXG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 21
AF528206/c
LOCUS       AF528206                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1112 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528206
VERSION     AF528206.1  GI:32810973
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1112"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87557.1"
                     /db_xref="GI:32810974"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLXG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 22
AF528207/c
LOCUS       AF528207                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC20 core antigen precursor, gene, partial cds.
ACCESSION   AF528207
VERSION     AF528207.1  GI:32810975
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
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            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC20"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87558.1"
                     /db_xref="GI:32810976"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 23
AF528208/c
LOCUS       AF528208                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC340 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528208
VERSION     AF528208.1  GI:32810977
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC340"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 24
AF528209/c
LOCUS       AF528209                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC58 core antigen precursor, gene, partial cds.
ACCESSION   AF528209
VERSION     AF528209.1  GI:32810978
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC58"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87559.1"
                     /db_xref="GI:32810979"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 25
AF528210/c
LOCUS       AF528210                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC470 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528210
VERSION     AF528210.1  GI:32810980
KEYWORDS    .
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SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC470"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 26
AF528211/c
LOCUS       AF528211                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC335 core antigen precursor, gene, partial cds.
ACCESSION   AF528211
VERSION     AF528211.1  GI:32810981
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC335"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87560.1"
                     /db_xref="GI:32810982"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 27
AF528212/c
LOCUS       AF528212                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC343 core antigen precursor, gene, partial cds.
ACCESSION   AF528212
VERSION     AF528212.1  GI:32810983
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC343"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87561.1"
                     /db_xref="GI:32810984"
                     /translation="MQLFHLCLIISCSCPTIQASKLCLGWLWG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 28
AF528213/c
LOCUS       AF528213                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC404 core antigen precursor, gene, partial cds.
ACCESSION   AF528213
VERSION     AF528213.1  GI:32810985
KEYWORDS    .
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SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC404"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87562.1"
                     /db_xref="GI:32810986"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 29
AF528214/c
LOCUS       AF528214                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC423 core antigen precursor, gene, partial cds.
ACCESSION   AF528214
VERSION     AF528214.1  GI:32810987
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
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                     /db_xref="taxon:10407"
                     /country="India"
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                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
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                     /db_xref="GI:32810988"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWD"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 30
AF528215/c
LOCUS       AF528215                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC424 core antigen precursor, gene, partial cds.
ACCESSION   AF528215
VERSION     AF528215.1  GI:32810989
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
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                     /isolate="ASC424"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
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                     /db_xref="GI:32810990"
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ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
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  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 31
AF528216/c
LOCUS       AF528216                150 bp    DNA     linear   VRL 31-JUL-2003
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DEFINITION  Hepatitis B virus ASC1035 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528216
VERSION     AF528216.1  GI:32810991
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
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                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
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                     /db_xref="GI:32810992"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
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  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 32
AF528217/c
LOCUS       AF528217                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1061 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528217
VERSION     AF528217.1  GI:32810993
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
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                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 33
AF528218/c
LOCUS       AF528218                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC339 core antigen precursor, gene, partial cds.
ACCESSION   AF528218
VERSION     AF528218.1  GI:32810994
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
                     /codon_start=1
                     /product="core antigen precursor"
                     /protein_id="AAP87566.1"
                     /db_xref="GI:32810995"
                     /translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
ORIGIN

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  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 34
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AF528219/c
LOCUS       AF528219                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC295 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528219
VERSION     AF528219.1  GI:32810996
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
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                     /proviral
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                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 35
AF528220/c
LOCUS       AF528220                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1027 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528220
VERSION     AF528220.1  GI:32810997
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /proviral
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                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
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ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 36
AF528221/c
LOCUS       AF528221                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1029 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528221
VERSION     AF528221.1  GI:32810998
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /proviral
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                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
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                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

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Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 37
AF528222/c
LOCUS       AF528222                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC298 core antigen precursor, gene, partial cds.
ACCESSION   AF528222
VERSION     AF528222.1  GI:32810999
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KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
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ORIGIN

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  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 38
AF528224/c
LOCUS       AF528224                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC263 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528224
VERSION     AF528224.1  GI:32811002
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 39
AF528225/c
LOCUS       AF528225                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1036 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528225
VERSION     AF528225.1  GI:32811003
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1036"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
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                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 40
AF528226/c
LOCUS       AF528226                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1062 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528226
VERSION     AF528226.1  GI:32811004
KEYWORDS    .
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SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
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                     /isolate="ASC1062"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 41
AF528227/c
LOCUS       AF528227               150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1065 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528227
VERSION     AF528227.1  GI:32811005
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /proviral
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                     /isolate="ASC1065"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
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Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 42
AF528228/c
LOCUS       AF528228               150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1072 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528228
VERSION     AF528228.1  GI:32811006
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1072"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 43
AF528229/c
LOCUS       AF528229               150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1074 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528229
VERSION     AF528229.1  GI:32811007
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
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  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="ASC1074"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

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  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 44
AF528231/c
LOCUS       AF528231                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1091 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528231
VERSION     AF528231.1  GI:32811009
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
                     /proviral
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                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
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     misc_feature    64. .>150
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                     core antigen precursor due to mutation"
ORIGIN

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Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 45
AF528232/c
LOCUS       AF528232                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC265 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528232
VERSION     AF528232.1  GI:32811010
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /proviral
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                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 150;
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  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 46
AF528233/c
LOCUS       AF528233                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC262 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528233
VERSION     AF528233.1  GI:32811011
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
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  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /proviral
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                     /isolate="ASC262"
                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

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  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 47
AF528234/c
LOCUS       AF528234                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1109 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528234
VERSION     AF528234.1  GI:32811012
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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                     /proviral
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                     /isolation_source="asymptomatic HBsAg carrier"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
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     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
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ORIGIN

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  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
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Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 48
AF528235/c
LOCUS       AF528235                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1275 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528235
VERSION     AF528235.1  GI:32811013
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
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                     /db_xref="taxon:10407"
                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
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ORIGIN

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  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 49
AF528236/c
LOCUS       AF528236                150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1274 nonfunctional core antigen precursor,
            gene, partial sequence.
ACCESSION   AF528236
VERSION     AF528236.1  GI:32811015
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
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  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
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                     /country="India"
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                     /note="contains partial basal core promoter"
     misc_feature    64. .>150
                     /note="contains complete precore region; nonfunctional
                     core antigen precursor due to mutation"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 150;
  Best Local Similarity   85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
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Db         96 AGAGATGATTAGGCAGAGGT 77


RESULT 50
AF528237/c
LOCUS       AF528237                 150 bp    DNA     linear   VRL 31-JUL-2003
DEFINITION  Hepatitis B virus ASC1090 core antigen precursor, gene, partial
            cds.
ACCESSION   AF528237
VERSION     AF528237.1  GI:32811016
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Comparative evaluation of HBV precore and basal core promoter
            mutants in Indian patients with diverse clinical manifestations
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150)
  AUTHORS   Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2002) Hepatitis Division, National Institute of
            Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Hepatitis B virus"
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                     /isolation_source="asymptomatic HBsAg carrier"
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                     /country="India"
     misc_feature    <1. .>150
                     /note="contains partial basal core promoter"
     CDS             64. .>150
                     /note="contains complete precore region"
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                     /product="core antigen precursor"
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ORIGIN

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  Best Local Similarity / 85.0%;  Pred. No. 15;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
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Db         96 AGAGATGATTAGGCAGAGGT 77


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Job time : 765 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 15, 2004, 09:10:16 ; Search time 181 Seconds
(without alignments)
580.047 Million cell updates/sec

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Perfect score: 20
Sequence: 1 agagaugauuaggcagaggt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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1: geneseqn1980s:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	2	AAT72560	Aat72560 Hepatitis
	2	20	100.0	20	2	AAT72561	Aat72561 Hepatitis
	3	20	100.0	25	3	AAA88131	Aaa88131 SP6 RNA p
c	4	20	100.0	27	4	AAH25416	Aah25416 Reverse P
	5	20	100.0	30	2	AAT72562	Aat72562 Hepatitis
	6	20	100.0	30	2	AAT72614	Aat72614 Hepatitis
	7	20	100.0	30	2	AAT72563	Aat72563 Hepatitis
	8	20	100.0	30	2	AAT72615	Aat72615 Hepatitis
c	9	20	100.0	39	10	ADC64742	Adc64742 Hepatitis
c	10	20	100.0	64	3	AAA88130	Aaa88130 SP6 RNA p
c	11	20	100.0	87	4	AAD09094	Aad09094 Hepatitis
c	12	20	100.0	129	4	AAD09093	Aad09093 Hepatitis
c	13	20	100.0	250	6	ABK29867	Abk29867 Wild type
c	14	20	100.0	639	6	AAD27422	Aad27422 Hepatitis
c	15	20	100.0	639	6	AAD31509	Aad31509 Hepatitis
c	16	20	100.0	646	12	ADL56756	Adl56756 HBV preco
c	17	20	100.0	655	2	AAQ47014	Aaq47014 HBV (adw)
c	18	20	100.0	655	2	AAT35649	Aat35649 Precore/c
c	19	20	100.0	655	4	AAH77569	Aah77569 HBV genot
c	20	20	100.0	655	4	AAH77568	Aah77568 HBV genot
c	21	20	100.0	655	4	AAH77574	Aah77574 HBV genot
c	22	20	100.0	655	4	AAH77573	Aah77573 HBV genot
c	23	20	100.0	655	4	AAH77570	Aah77570 HBV genot
c	24	20	100.0	655	4	AAH77571	Aah77571 HBV genot
c	25	20	100.0	655	4	AAD21244	Aad21244 Hepatitis
c	26	20	100.0	655	9	ABX80077	Abx80077 Hepatitis
c	27	20	100.0	655	10	ABX96938	Abx96938 Hepatitis
c	28	20	100.0	660	1	AAN91081	Aan91081 DNA seque
c	29	20	100.0	664	4	AAH77572	Aah77572 HBV genot
c	30	20	100.0	669	12	ADO07220	Ado07220 Hepatitis
c	31	20	100.0	673	4	AAD09092	Aad09092 Hepatitis
c	32	20	100.0	675	4	AAH77563	Aah77563 HBV preCo
c	33	20	100.0	681	4	AAH77566	Aah77566 HBV genot
c	34	20	100.0	681	4	AAH77567	Aah77567 HBV genot
c	35	20	100.0	750	1	AAN80943	Aan80943 HBV core
c	36	20	100.0	909	6	AAH77169	Aah77169 Regulator
c	37	20	100.0	1334	2	AAV82691	Aav82691 Fulminant
c	38	20	100.0	1395	2	AAV82688	Aav82688 Fulminant
c	39	20	100.0	1400	2	AAV82687	Aav82687 Fulminant
c	40	20	100.0	1445	2	AAV82692	Aav82692 Fulminant
c	41	20	100.0	1445	2	AAV82685	Aav82685 Fulminant
c	42	20	100.0	1445	2	AAV82690	Aav82690 Fulminant
c	43	20	100.0	1445	2	AAV82684	Aav82684 Fulminant
c	44	20	100.0	1500	2	AAV82695	Aav82695 Fulminant
c	45	20	100.0	1500	2	AAV82683	Aav82683 Fulminant
c	46	20	100.0	1500	2	AAV82694	Aav82694 Fulminant
c	47	20	100.0	1500	2	AAV82686	Aav82686 Fulminant
c	48	20	100.0	1500	2	AAV82706	Aav82706 Wild type
c	49	20	100.0	1500	2	AAV82689	Aav82689 Fulminant
c	50	20	100.0	1500	2	AAV82693	Aav82693 Fulminant
c	51	20	100.0	1977	12	ADJ53703	Adj53703 RNA pseud
c	52	20	100.0	2342	1	AAN93072	Aan93072 Sequence
c	53	20	100.0	2743	1	AAN00003	Aan00003 Sequence
c	54	20	100.0	2743	2	AAQ04799	Aaq04799 Recombina
c	55	20	100.0	3180	4	AAH42375	Aah42375 Nucleotid
c	56	20	100.0	3182	6	AAD31765	Aad31765 Hepatitis
c	57	20	100.0	3182	9	ACA62422	Aca62422 Hepatitis
c	58	20	100.0	3182	10	AAD60866	Aad60866 Hepatitis
c	59	20	100.0	3183	1	AAN30035	Aan30035 DNA contg
c	60	20	100.0	3200	1	AAN40243	Aan40243 DNA encod
c	61	20	100.0	3200	1	AAN70165	Aan70165 Entire nu
c	62	20	100.0	3220	3	AAZ88924	Aaz88924 Hepatitis
c	63	20	100.0	3221	2	AAZ23281	Aaz23281 DNA seque
c	64	20	100.0	3221	4	AAH42374	Aah42374 Nucleotid
c	65	20	100.0	3221	6	ABK23902	Abk23902 Bee venom
c	66	20	100.0	3221	6	ABS70986	Abs70986 DNA encod
c	67	20	100.0	3221	6	ABS66412	Abs66412 Hepatitis
c	68	20	100.0	3221	10	ADD27773	Add27773 HBV subty
c	69	20	100.0	3248	4	AAD09091	Aad09091 Hepatitis
c	70	20	100.0	3248	4	AAH77562	Aah77562 HBV genot
c	71	20	100.0	4084	4	AAD14316	Aad14316 Hepatitis
c	72	20	100.0	4496	4	AAD14317	Aad14317 Hepatitis
c	73	20	100.0	5618	2	AAQ88310	Aaq88310 Plasmid p
c	74	20	100.0	5639	2	AAX57972	Aax57972 Recombina
c	75	20	100.0	6371	2	AAZ23292	Aaz23292 DNA seque
c	76	20	100.0	6371	2	AAZ23285	Aaz23285 DNA seque
c	77	20	100.0	6375	2	AAZ23294	Aaz23294 DNA seque
c	78	20	100.0	7991	6	AAS16094	Aas16094 HBV viral
c	79	20	100.0	8007	6	AAS16092	Aas16092 HBV viral
c	80	20	100.0	8717	6	AAS16093	Aas16093 HBV viral
c	81	20	100.0	9325	2	AAZ23282	Aaz23282 DNA seque
	82	20	100.0	9534	2	AAT62072	Aat62072 Vector RP
c	83	20	100.0	9859	2	AAZ23286	Aaz23286 DNA seque
c	84	19.6	98.0	33	12	ADM16809	Adm16809 Hepatitis
c	85	19.2	96.0	30	2	AAQ45797	Aaq45797 HBV ampli
c	86	19.2	96.0	30	2	AAV07794	Aav07794 HBV.D44 a
c	87	19.2	96.0	30	2	AAV83023	Aav83023 Amplifier
	88	19.2	96.0	50	2	AAQ06722	Aaq06722 :HBV.LLA2
c	89	19	95.0	19	11	ADL99951	Adl99951 Hepatitis
	90	19	95.0	19	11	ADM00598	Adm00598 Hepatitis
c	91	19	95.0	20	2	AAQ37777	Aaq37777 Probe PR1
c	92	19	95.0	20	5	AAC88880	Aac88880 HBV polyA
c	93	19	95.0	20	6	ABT08252	Abt08252 Human ade
c	94	19	95.0	20	12	ADF09463	Adf09463 E1-delete

c 95	19	95.0	22	2	AAT73885	Aat73885 Human hep
c 96	19	95.0	87	2	AAT05545	Aat05545 Human hep
c 97	19	95.0	94	2	AAT73892	Aat73892 Human hep
c 98	19	95.0	94	2	AAT73890	Aat73890 Human hep
c 99	19	95.0	94	2	AAT73887	Aat73887 Human hep
c 100	19	95.0	94	2	AAT73889	Aat73889 Human hep

ALIGNMENTS

RESULT 1
AAT72560
ID AAT72560 standard; DNA; 20 BP.
XX
AC AAT72560;
XX
DT 03-SEP-1997 (first entry)
XX
DE Hepatitis B virus RNA antisense oligonucleotide HBV43a.
XX
KW HBV; HBV infection; inhibition; replication; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .20
FT /*tag= a
FT /note= "Internucleotide linkages are phosphorothioate"
XX
PN WO9639502-A1.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002432.
XX
PR 06-JUN-1995; 95US-00467397.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
PI Craig CJ, Frank BL, Goodchild J, Jupp R, Kilkuskie RE, Mills JS;
PI Roberts NA, Roberts PC, Slade A;
XX
DR WPI; 1997-043124/04.
XX
PT Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT used in the detection and treatment of HBV infection.
XX
PS Claim 1; Page 12; 81pp; English.
XX
CC The present sequence represents a synthetic oligonucleotide HBV43a which
CC is complementary to a portion of the hepatitis B virus (HBV) RNA. The
CC antisense oligonucleotide may be used to detect the presence of HBV in a
CC sample. The antisense oligonucleotide, and oligonucleotides containing a
CC sequence which is complementary to at least two non- contiguous regions
CC of an HBV nucleic acid, may be used for inhibiting HBV replication in a
CC cell or for the treatment of HBV infection
XX
SQ Sequence 20 BP; 7 A; 1 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.8;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db          1 AGAGATGATTAGGCAGAGGT 20
```

RESULT 2
AAT72561
ID AAT72561 standard; DNA; 20 BP.
XX
AC AAT72561;
XX
DT 03-SEP-1997 (first entry)
XX
DE Hepatitis B virus RNA antisense oligonucleotide HBV43Ma.
XX
KW HBV; HBV infection; inhibition; replication; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .20
FT /*tag= a
FT /note= "Internucleotide linkages are phosphorothioate"
FT misc_RNA 1. .10
FT /*tag= b
FT /note= "2'-OMe RNA"
FT modified_base 1
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methyladenosine"
FT modified_base 2
FT /*tag= d
FT /mod_base= gm
FT modified_base 3
FT /*tag= e
FT /mod_base= OTHER
FT /note= "2'-O-methyladenosine"
FT modified_base 4
FT /*tag= f
FT /mod_base= gm
FT modified_base 5
FT /*tag= g
FT /mod_base= OTHER
FT /note= "2'-O-methyladenosine"
FT modified_base 6
FT /*tag= h
FT /mod_base= um
FT modified_base 7
FT /*tag= i
FT /mod_base= gm
FT modified_base 8
FT /*tag= j
FT /mod_base= OTHER
FT /note= "2'-O-methyladenosine"
FT modified_base 9
FT /*tag= k
FT /mod_base= um
FT modified_base 10
FT /*tag= l
FT /mod_base= um
XX
PN WO9639502-A1.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002432.
XX
PR 06-JUN-1995; 95US-00467397.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
PI Craig CJ, Frank BL, Goodchild J, Jupp R, Kilkuskie RE, Mills JS;
PI Roberts NA, Roberts PC, Slade A;
XX
DR WPI; 1997-043124/04.
XX
PT Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT used in the detection and treatment of HBV infection.
XX
PS Claim 1; Page 12; 81pp; English.

```
XX
CC   The present sequence represents a synthetic oligonucleotide HBV43Ma which
CC   is complementary to a portion of the hepatitis B virus (HBV) RNA. The
CC   antisense oligonucleotide may be used to detect the presence of HBV in a
CC   sample. The antisense oligonucleotide, and oligonucleotides containing a
CC   sequence which is complementary to at least two non- contiguous regions
CC   of an HBV nucleic acid, may be used for inhibiting HBV replication in a
CC   cell or for the treatment of HBV infection
XX
SQ   Sequence 20 BP; 7 A; 1 C; 8 G; 1 T; 3 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              ||||||||||||||||||||
Db          1 AGAGAUGAUUAGGCAGAGGT 20


RESULT 3
AAA88131
ID   AAA88131 standard; RNA; 25 BP.
XX
AC   AAA88131;
XX
DT   15-SEP-2003  (revised)
DT   13-DEC-2000  (first entry)
XX
DE   SP6 RNA polymerase promoter sequence SEQ ID NO:3.
XX
KW   Hepatitis B virus; HBV; detection; probe; promoter; ss.
XX
OS   Enterobacteria phage SP6.
XX
PN   US6100024-A.
XX
PD   08-AUG-2000.
XX
PF   08-FEB-1991;   91US-00652888.
XX
PR   08-FEB-1991;   91US-00652888.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Hudson GR,  Dimond RL,  Schumm JW;
XX
DR   WPI; 2000-542420/49.
XX
PT   Single-stranded DNA probe comprising an anti-target nucleic acid, a (-)-
PT   promoter segment linked to the anti-target segment and a reporter
PT   segment, useful for detecting a target nucleic acid, e.g. hepatitis B
PT   virus, in a sample.
XX
PS   Example 3; Col 19-20; 18pp; English.
XX
CC   The present invention describes a single-stranded DNA probe (I)
CC   comprising in 3'-5' order, an anti-target nucleic acid segment, a (-)-
CC   promoter segment functionally linked to the anti-target segment, and a
CC   nucleic acid reporter segment. The probe is useful for testing a sample
CC   of a nucleic acid for the presence of a target nucleic acid segment or
CC   for detecting a target nucleic acid segment in a sample. The probe may
CC   also be used for the detection of hepatitis B virus (HBV). The present
CC   sequence represents a bacteriophage SP6 RNA polymerase promoter sequence
CC   which is used in an example from the present invention. (Updated on 15-
CC   SEP-2003 to standardise OS field)
XX
SQ   Sequence 25 BP; 10 A; 1 C; 10 G; 0 T; 4 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 3;  Length 25;
  Best Local Similarity   95.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              ||||||||||||||||||||:
Db          3 AGAGAUGAUUAGGCAGAGGU 22


RESULT 4
AAH25416/c
ID   AAH25416 standard; DNA; 27 BP.
XX
AC   AAH25416;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Reverse PCR primer used to amplify a HBV DNA fragment.
XX
KW   Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   27
FT                   /*tag=  a
FT                   /note= "derivatisation with a p-(t-butyl)benzyl-residue"
XX
PN   WO200137291-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP011459.
XX
PR   17-NOV-1999;   99EP-00122853.
PR   12-MAY-2000; 2000EP-00110165.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Weindel K,  Riedling M,  Geiger A;
XX
DR   WPI; 2001-381247/40.
XX
PT   Novel composition of magnetic glass particles for purification of DNA or
PT   RNA in automated processes.
XX
PS   Example 7; Page 99; 105pp; English.
XX
CC   The specification describes a composition of magnetic glass particles,
CC   which contain at least one magnetic object with a mean diameter between 5
CC   -500 nm. The composition is useful for the purification of nucleic acids.
CC   The composition can be used to process large quantities of nucleic acid
CC   samples, because it does not involve the particles being centrifuged or
CC   the fluids being drawn through glass fiber filters. PCR primers AAH25415-
CC   16 were used to amplify HBV DNA fragments. The amplified fragment can be
CC   purified using the method of the invention
XX
SQ   Sequence 27 BP; 5 A; 10 C; 2 G; 10 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 27;
  Best Local Similarity   85.0%;  Pred. No. 6;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         21 AGAGATGATTAGGCAGAGGT 2


RESULT 5
AAT72562
ID   AAT72562 standard; DNA; 30 BP.
XX
AC   AAT72562;
XX
DT   03-SEP-1997  (first entry)
XX
DE   Hepatitis B virus RNA antisense oligonucleotide HBV88b.
```

```
XX
KW   HBV; HBV infection; inhibition; replication; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .30
FT                   /*tag= a
FT                   /note= "Internucleotide linkages are phosphorothioate"
XX
PN   WO9639502-A1.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002432.
XX
PR   06-JUN-1995;   95US-00467397.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Craig CJ,  Frank BL,  Goodchild J,  Jupp R,  Kilkuskie RE,  Mills JS;
PI   Roberts NA,  Roberts PC,  Slade A;
XX
DR   WPI; 1997-043124/04.
XX
PT   Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT   used in the detection and treatment of HBV infection.
XX
PS   Claim 1; Page 12; 81pp; English.
XX
CC   The present sequence represents a synthetic oligonucleotide HBV88b which
CC   is complementary to a portion of the hepatitis B virus (HBV) RNA. The
CC   antisense oligonucleotide may be used to detect the presence of HBV in a
CC   sample. The antisense oligonucleotide, and oligonucleotides containing a
CC   sequence which is complementary to at least two non- contiguous regions
CC   of an HBV nucleic acid, may be used for inhibiting HBV replication in a
CC   cell or for the treatment of HBV infection
XX
SQ   Sequence 30 BP; 12 A; 3 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   85.0%;  Pred. No. 6;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         11 AGAGATGATTAGGCAGAGGT 30


RESULT 6
AAT72614
ID   AAT72614 standard; DNA; 30 BP.
XX
AC   AAT72614;
XX
DT   04-SEP-1997  (first entry)
XX
DE   Hepatitis B virus RNA antisense oligonucleotide HBV-87b.
XX
KW   HBV; HBV infection; inhibition; replication; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .30
FT                   /*tag= a
FT                   /note= "Internucleotide linkages are phosphorothioate"
XX
PN   WO9639502-A1.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002432.
XX
PR   06-JUN-1995;   95US-00467397.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Craig CJ,  Frank BL,  Goodchild J,  Jupp R,  Kilkuskie RE,  Mills JS;
PI   Roberts NA,  Roberts PC,  Slade A;
XX
DR   WPI; 1997-043124/04.
XX
PT   Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT   used in the detection and treatment of HBV infection.
XX
PS   Claim 5; Page 15; 81pp; English.
XX
CC   The present sequence represents a synthetic oligonucleotide HBV-87b which
CC   contains a sequence which is complementary to at least two non-contiguous
CC   regions of a hepatitis B virus (HBV) nucleic acid. The antisense
CC   oligonucleotide may be used to detect the presence of HBV in a sample.
CC   The antisense oligonucleotide, and oligonucleotides complementary to a
CC   portion of the HBV RNA, may be used for inhibiting HBV replication in a
CC   cell or for the treatment of HBV infection
XX
SQ   Sequence 30 BP; 10 A; 2 C; 12 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   85.0%;  Pred. No. 6;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db          1 AGAGATGATTAGGCAGAGGT 20


RESULT 7
AAT72563
ID   AAT72563 standard; DNA; 30 BP.
XX
AC   AAT72563;
XX
DT   03-SEP-1997  (first entry)
XX
DE   Hepatitis B virus RNA antisense oligonucleotide HBV88Mb.
XX
KW   HBV; HBV infection; inhibition; replication; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .30
FT                   /*tag= a
FT                   /note= "Internucleotide linkages are phosphorothioate"
FT   misc_RNA        1. .20
FT                   /*tag= b
FT                   /note= "2'-OMe RNA"
FT   modified_base   1
FT                   /*tag= c
FT                   /mod_base= gm
FT   modified_base   2
FT                   /*tag= d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   3
FT                   /*tag= e
FT                   /mod_base= cm
FT   modified_base   4
FT                   /*tag= f
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   5
FT                   /*tag= g
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FT                  /mod_base= um
FT   modified_base  6
FT                  /*tag=  h
FT                  /mod_base= gm
FT   modified_base  7
FT                  /*tag=  i
FT                  /mod_base= OTHER
FT                  /note= "2'-O-methyladenosine"
FT   modified_base  8
FT                  /*tag=  j
FT                  /mod_base= OTHER
FT                  /note= "2'-O-methyladenosine"
FT   modified_base  9
FT                  /*tag=  k
FT                  /mod_base= cm
FT   modified_base  10
FT                  /*tag=  l
FT                  /mod_base= OTHER
FT                  /note= "2'-O-methyladenosine"
FT   modified_base  11
FT                  /*tag=  m
FT                  /mod_base= OTHER
FT                  /note= "2'-O-methyladenosine"
FT   modified_base  12
FT                  /*tag=  n
FT                  /mod_base= gm
FT   modified_base  13
FT                  /*tag=  o
FT                  /mod_base= OTHER
FT                  /note= "2'-O-methyladenosine"
FT   modified_base  14
FT                  /*tag=  p
FT                  /mod_base= gm
FT   modified_base  15
FT                  /*tag=  q
FT                  /mod_base= OTHER
FT                  /note= "2'-O-methyladenosine"
FT   modified_base  16
FT                  /*tag=  r
FT                  /mod_base= um
FT   modified_base  17
FT                  /*tag=  s
FT                  /mod_base= gm
FT   modified_base  18
FT                  /*tag=  s
FT                  /mod_base= OTHER
FT                  /note= "2'-O-methyladenosine"
FT   modified_base  19
FT                  /*tag=  u
FT                  /mod_base= um
FT   modified_base  20
FT                  /*tag=  v
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XX
PN   WO9639502-A1.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002432.
XX
PR   06-JUN-1995;   95US-00467397.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Craig CJ,  Frank BL,  Goodchild J,  Jupp R,  Kilkuskie RE,  Mills JS;
PI   Roberts NA,  Roberts PC,  Slade A;
XX
DR   WPI; 1997-043124/04.
XX
PT   Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT   used in the detection and treatment of HBV infection.
XX
PS   Claim 1; Page 12; 81pp; English.
XX
CC   The present sequence represents a synthetic oligonucleotide HBV88Mb which
CC   is complementary to a portion of the hepatitis B virus (HBV) RNA. The
CC   antisense oligonucleotide may be used to detect the presence of HBV in a
CC   sample. The antisense oligonucleotide, and oligonucleotides containing a
CC   sequence which is complementary to at least two non- contiguous regions
CC   of an HBV nucleic acid, may be used for inhibiting HBV replication in a
CC   cell or for the treatment of HBV infection
XX
SQ   Sequence 30 BP; 12 A; 3 C; 10 G; 1 T; 4 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              ||||||||||||||||||||
Db         11 AGAGAUGAUUAGGCAGAGGT 30


RESULT 8
AAT72615
ID   AAT72615 standard; DNA; 30 BP.
XX
AC   AAT72615;
XX
DT   04-SEP-1997  (first entry)
XX
DE   Hepatitis B virus RNA antisense oligonucleotide HBV-87Mb.
XX
KW   HBV; HBV infection; inhibition; replication; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .30
FT                   /*tag=  a
FT                   /note= "Internucleotide linkages are phosphorothioate"
FT   misc_RNA        1. .10
FT                   /*tag=  b
FT                   /note= "2'-OMe RNA"
FT   modified_base   1
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   2
FT                   /*tag=  d
FT                   /mod_base= gm
FT   modified_base   3
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   4
FT                   /*tag=  f
FT                   /mod_base= gm
FT   modified_base   5
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   6
FT                   /*tag=  h
FT                   /mod_base= um
FT   modified_base   7
FT                   /*tag=  i
FT                   /mod_base= gm
FT   modified_base   8
FT                   /*tag=  j
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyladenosine"
FT   modified_base   9
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FT   modified_base   10
FT                   /*tag=  1
FT                   /mod_base= um
XX
PN   WO9639502-A1.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002432.
XX
PR   06-JUN-1995;   95US-00467397.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Craig CJ,  Frank BL,  Goodchild J,  Jupp R,  Kilkuskie RE,  Mills JS;
PI   Roberts NA,  Roberts PC,  Slade A;
XX
DR   WPI; 1997-043124/04.
XX
PT   Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences -
PT   used in the detection and treatment of HBV infection.
XX
PS   Claim 5; Page 15; 81pp; English.
XX
CC   The present sequence represents a synthetic oligonucleotide HBV-87Mb
CC   which contains a sequence which is complementary to at least two non-
CC   contiguous regions of a hepatitis B virus (HBV) nucleic acid. The
CC   antisense oligonucleotide may be used to detect the presence of HBV in a
CC   sample. The antisense oligonucleotide, and oligonucleotides complementary
CC   to a portion of the HBV RNA, may be used for inhibiting HBV replication
CC   in a cell or for the treatment of HBV infection
XX
SQ   Sequence 30 BP; 10 A; 2 C; 12 G; 3 T; 3 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              ||||||||||||||||||||
Db          1 AGAGAUGAUUAGGCAGAGGT 20


RESULT 9
ADC64742/c
ID   ADC64742 standard; RNA; 39 BP.
XX
AC   ADC64742;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Hepatitis B virus DNA polymerase related RNA oligonucleotide.
XX
KW   screening; antiviral; hepatitis B virus; HBV; DNA polymerase; ss.
XX
OS   Synthetic.
OS   Hepatitis B virus.
XX
PN   KR2002007891-A.
XX
PD   29-JAN-2002.
XX
PF   19-JUL-2000; 2000KR-00041420.
XX
PR   19-JUL-2000; 2000KR-00041420.
XX
PA   (MOGA-) MOGAM BIOTECHNOLOGY INST.
PA   (VIRO-) VIROGEN CO LTD.
XX
PI   Ji HJ,  Jung SI,  Kim YC,  Min MG,  Ryu WS,  Yoon GS;
XX
DR   WPI; 2003-309015/30.
XX
PT   Screening of antiviral agents by protein-priming activity of hepatitis B
PT   virus DNA polymerase.
XX
PS   Disclosure; Page 12; 13pp; Korean.
XX
CC   The present invention describes a method of screening for an antiviral
CC   agent by the protein-priming activity of hepatitis B virus (HBV) DNA
CC   polymerase. Also described is developing an antiviral agent with a high
CC   selectivity to HBV which can be used for high-throughput screening. The
CC   present sequence represents an RNA oligonucleotide which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 39 BP; 5 A; 13 C; 3 G; 0 T; 18 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 10;  Length 39;
  Best Local Similarity  85.0%;  Pred. No. 6.2;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         27 AGAGATGATTAGGCAGAGGT 8


RESULT 10
AAA88130/c
ID   AAA88130 standard; DNA; 64 BP.
XX
AC   AAA88130;
XX
DT   15-SEP-2003  (revised)
DT   13-DEC-2000  (first entry)
XX
DE   SP6 RNA polymerase promoter sequence SEQ ID NO:2.
XX
KW   Hepatitis B virus; HBV; detection; probe; promoter; ds.
XX
OS   Enterobacteria phage SP6.
XX
PN   US6100024-A.
XX
PD   08-AUG-2000.
XX
PF   08-FEB-1991;   91US-00652888.
XX
PR   08-FEB-1991;   91US-00652888.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Hudson GR,  Dimond RL,  Schumm JW;
XX
DR   WPI; 2000-542420/49.
XX
PT   Single-stranded DNA probe comprising an anti-target nucleic acid, a (-)-
PT   promoter segment linked to the anti-target segment and a reporter
PT   segment, useful for detecting a target nucleic acid, e.g. hepatitis B
PT   virus, in a sample.
XX
PS   Example 3; Col 19-20; 18pp; English.
XX
CC   The present invention describes a single-stranded DNA probe (I)
CC   comprising in 3'-5' order, an anti-target nucleic acid segment, a (-)-
CC   promoter segment functionally linked to the anti-target segment, and a
CC   nucleic acid reporter segment. The probe is useful for testing a sample
CC   of a nucleic acid for the presence of a target nucleic acid segment or
CC   for detecting a target nucleic acid segment in a sample. The probe may
CC   also be used for the detection of hepatitis B virus (HBV). The present
CC   sequence represents a bacteriophage SP6 RNA polymerase promoter sequence
CC   which is used in an example from the present invention. (Updated on 15-
CC   SEP-2003 to standardise OS field)
XX
SQ   Sequence 64 BP; 14 A; 22 C; 4 G; 24 T; 0 U; 0 Other;
```

```
  Query Match           100.0%;  Score 20;  DB 3;  Length 64;
  Best Local Similarity   85.0%;  Pred. No. 6.6;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         23 AGAGATGATTAGGCAGAGGT 4


RESULT 11
AAD09094/c
ID   AAD09094 standard; DNA; 87 BP.
XX
AC   AAD09094;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Hepatitis B virus FR1 strain genotype G HBeAg DNA fragment.
XX
KW   HBV genotype G; precore; HBpol; polymerase; envelope protein; preS1;
KW   preS2; surface antigen; HBsAg; HBX protein; vaccine; HBeAg;
KW   liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200138498-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US032108.
XX
PR   24-NOV-1999;   99US-0167206P.
XX
PA   (PHAR-) PHARMASSET INC.
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Schinazi R,  De Gendt S,  Van Geyt C,  Zoulim F,  Fried M;
PI   Rossau R;
XX
DR   WPI; 2001-367676/38.
XX
PT   Novel hepatitis B virus genotype G, nucleic acids encoding virus,
PT   polypeptides encoded by nucleic acids, useful for preparing vaccine to
PT   treat or prevent the hepatitis B virus genotype G infection in a subject.
XX
PS   Claim 6; Page 57; 84pp; English.
XX
CC   The present invention relates to hepatitis B virus (HBV) strain FR1,
CC   genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1,
CC   PreS2 and surface antigen HBsAg) and HBX proteins. HBV genotype G nucleic
CC   acids and polypeptides are useful for diagnosing, prognosing and treating
CC   infections caused by HBV genotype G. They can be used in a vaccine to
CC   treat or prevent HBV genotype G infection. The HBV genotype G derived
CC   nucleic acids and antibodies are useful for detecting HBV genotype G in a
CC   sample or diagnosis of HBV genotype G infection. The presence of HBV
CC   genotype G statistically correlates with the presence of liver damage
CC   and/or liver cancer in the subject. The HBV genotype G core insert
CC   peptide encoding nucleic acid is useful for designing monitoring assays
CC   to study and predict the evolution of anti-HBe and anti-HBc antibodies
CC   and HBeAg (genotype G e antigen) in patients infected with HBV. The
CC   antibodies or antigens of HBV genotype G are useful for identifying a
CC   stage of liver disease caused by HBV genotype G. The present sequence is
CC   a hepatitis B virus (HBV) strain FR1, genotype G DNA fragment encoding e
CC   antigen (HBeAg)
XX
SQ   Sequence 87 BP; 14 A; 24 C; 17 G; 32 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 4;  Length 87;
  Best Local Similarity   85.0%;  Pred. No. 6.8;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 12
AAD09093/c
ID   AAD09093 standard; DNA; 129 BP.
XX
AC   AAD09093;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Hepatitis B virus FR1 strain genotype G DNA fragment #1.
XX
KW   HBV genotype G; precore; HBpol; polymerase; envelope protein; preS1;
KW   preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease;
KW   hepatitis; liver cancer; HBcAg; core antigen; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200138498-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US032108.
XX
PR   24-NOV-1999;   99US-0167206P.
XX
PA   (PHAR-) PHARMASSET INC.
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Schinazi R,  De Gendt S,  Van Geyt C,  Zoulim F,  Fried M;
PI   Rossau R;
XX
DR   WPI; 2001-367676/38.
XX
PT   Novel hepatitis B virus genotype G, nucleic acids encoding virus,
PT   polypeptides encoded by nucleic acids, useful for preparing vaccine to
PT   treat or prevent the hepatitis B virus genotype G infection in a subject.
XX
PS   Claim 5; Page 57; 84pp; English.
XX
CC   The present invention relates to hepatitis B virus (HBV) strain FR1,
CC   genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1,
CC   PreS2 and surface antigen HBsAg) and HBX proteins. HBV genotype G nucleic
CC   acids and polypeptides are useful for diagnosing, prognosing and treating
CC   infections caused by HBV genotype G. They can be used in a vaccine to
CC   treat or prevent HBV genotype G infection. The HBV genotype G derived
CC   nucleic acids and antibodies are useful for detecting HBV genotype G in a
CC   sample or diagnosis of HBV genotype G infection. The presence of HBV
CC   genotype G statistically correlates with the presence of liver damage
CC   and/or liver cancer in the subject. The HBV genotype G core insert
CC   peptide encoding nucleic acid is useful for designing monitoring assays
CC   to study and predict the evolution of anti-HBe and anti-HBc antibodies
CC   and HBeAg (genotype G e antigen) in patients infected with HBV. The
CC   antibodies or antigens of HBV genotype G are useful for identifying a
CC   stage of liver disease caused by HBV genotype G. The present sequence is
CC   a hepatitis B virus (HBV) strain FR1, genotype G DNA fragment
XX
SQ   Sequence 129 BP; 25 A; 32 C; 26 G; 46 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 4;  Length 129;
  Best Local Similarity   85.0%;  Pred. No. 7.1;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 13
ABK29867/c
ID   ABK29867 standard; DNA; 250 BP.
XX
```

```
AC   ABK29867;
XX
DT   23-APR-2002  (first entry)
XX
DE   Wild type hepatitis B virus core promoter.
XX
KW   Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
KW   HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
KW   vanH promoter; androgen receptor promoter; AR promoter;
KW   human epidermal growth factor receptor 2 promoter; her2 promoter;
KW   beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
KW   colon cancer; immunological disorder; prostate cancer; cytostatic;
KW   autoimmune disease; HBV pre-S promoter; HBV-X promoter;
KW   Enterococcus infection; immunosuppressive; antibacterial; antiviral;
KW   gene expression modulator; multiple sclerosis; MS;
KW   chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
KW   systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
KW   familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
KW   transgenic; ds.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    61. .72
FT                   /*tag=  a
FT                   /bound_moiety= "HNF4"
FT                   /note= "Hepatocyte nuclear factor 4"
FT   misc_binding    80. .90
FT                   /*tag=  b
FT                   /bound_moiety= "HNF3-1"
FT                   /note= "Hepatocyte nuclear factor 3-1"
FT   misc_binding    115. .126
FT                   /*tag=  c
FT                   /bound_moiety= "HNF3-2"
FT                   /note= "Hepatocyte nuclear factor 3-2"
XX
PN   WO200194600-A2.
XX
PD   13-DEC-2001.
XX
PF   06-JUN-2001; 2001WO-US018343.
XX
PR   06-JUN-2000; 2000US-0209549P.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Kim JP,  Starr DB,  Tam AW,  Laurance ME,  Michelotti EF;
PI   Velligan MD,  Latour DR,  Thomas RL,  Kongpachith A,  Sheppard LT;
PI   Lim MY,  Bruice TW;
XX
DR   WPI; 2002-130595/17.
XX
PT   New nucleic acid regulatory sequences, which are able to regulate
PT   expression of a gene operably linked to a promoter, useful for regulating
PT   the expression of transgenes and for treating e.g., cancer and
PT   immunological diseases.
XX
PS   Disclosure; Fig 1A; 95pp; English.
XX
CC   The invention describes an isolated nucleic acid regulatory sequence for
CC   a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
CC   (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
CC   epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
CC   (Bla) promoter. Transcription regulatory sequences may be used to
CC   regulate expression of the endogenous, autologous or heterologous genes
CC   operably linked to the promoter, and may be incorporated into
CC   heterologous nucleic acid constructs for use in regulated expression of
CC   transgenes. Regulated expression of cyclin D1 can be used in cancer
CC   therapies, such as breast, colon or pancreatic cancers and familial
CC   adenomatous polyposis. Regulation of the activity of CD40L gene promoter
CC   may be used in the treatment of immunological disorders, such as
CC   autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
CC   erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
CC   arthritis. Regulated expression of genes under the control of the HBV
CC   (hepatitis B)-specific core, pre-S and X promoters can be used in the
CC   therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
CC   hepatocellular carcinoma, and in the regulated expression of liver cell-
CC   specific genes. Regulated expression of the vanH gene promoter can be
CC   used in treatment of Enterococcus infection, while regulated expression
CC   of the androgen receptor gene can be used in the treatment of prostate
CC   cancer. This sequence represents the hepatitis B virus core promoter the
CC   regulatory regions of which are described in the method of the invention
XX
SQ   Sequence 250 BP; 66 A; 59 C; 62 G; 63 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 250;
  Best Local Similarity   85.0%;  Pred. No. 7.6;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        248 AGAGATGATTAGGCAGAGGT 229


RESULT 14
AAD27422/c
ID   AAD27422 standard; DNA; 639 BP.
XX
AC   AAD27422;
XX
DT   18-APR-2002  (first entry)
XX
DE   Hepatitis B virus (HBV) core antigen (HBcAg) encoding DNA #1.
XX
KW   Hepatitis B virus; HBV; core antigen; HBcAg; immune system; typhoid;
KW   prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes;
KW   hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea;
KW   tuberculosis; polio; rabies; acquired immunodeficiency syndrome; AIDS;
KW   dengue fever; yellow fever; malaria; whooping cough; salmonellosis;
KW   food poisoning; meningitis; gonorrhea; antiviral; antibacterial;
KW   antiprotozoal; ds.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .639
FT                   /*tag=  a
FT                   /product= "HBcAg"
XX
PN   WO200198333-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-GB002817.
XX
PR   22-JUN-2000; 2000GB-00015308.
PR   06-OCT-2000; 2000GB-00024544.
XX
PA   (CELL-) CELLTECH PHARM LTD.
XX
PI   Page M,  Li J,  Pumpens P;
XX
DR   WPI; 2002-098223/13.
DR   P-PSDB; AAE17018.
XX
PT   New proteins comprising a modified hepatitis B core antigen, useful as a
PT   vaccine in prophylactic or therapeutic vaccination of the human or animal
PT   body, particularly against hepatitis B virus infection.
XX
PS   Disclosure; Page 38-39; 40pp; English.
XX
CC   The invention relates to modified proteins comprising hepatitis B virus
CC   (HBV) core antigen (HBcAg) wherein one or more of the four arginine
CC   repeats has been deleted and the protein comprising the C-terminal
CC   cysteine of HBcAg. The deleted region may be replaced by an epitope from
CC   a protein other than HBcAg, in which case the HBcAg acts as a carrier to
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CC present the epitope to the immune system. This chimeric protein or its
CC nucleic acid is useful as a vaccine or in a method of prophylactic or
CC therapeutic vaccination of the human or animal body, particularly against
CC HBV. The nucleic acid encoding the protein may be used in gene therapy or
CC DNA vaccination protocols. The chimeric protein or its nucleic acid may
CC also be used as the basis of a prophylactic vaccine against a range of
CC diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV),
CC influenza, foot-and-mouth disease, polio, herpes, rabies, acquired
CC immunodeficiency syndrome (AIDS), dengue fever, yellow fever, malaria,
CC tuberculosis, whooping cough, salmonellosis, typhoid, food poisoning,
CC diarrhoea, meningitis or gonorrhea. The present sequence is a DNA
CC encoding Hepatitis B virus core antigen (HBcAg)
XX
SQ Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 639;
Best Local Similarity 85.0%; Pred. No. 8.4;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGAUGAUUAGGCAGAGGT 20
||||||:||::||||||||||
Db 33 AGAGATGATTAGGCAGAGGT 14

RESULT 15
AAD31509/c
ID AAD31509 standard; DNA; 639 BP.
XX
AC AAD31509;
XX
DT 18-JUN-2002 (first entry)
XX
DE Hepatitis B virus core antigen (HBcAg) encoding DNA.
XX
KW Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis;
KW therapeutic; vaccine; acquired immune deficiency syndrome; influenza;
KW polio; herpes; rabies; AIDS; foot-and-mouth disease; ds.
XX
OS Hepatitis B virus.
XX
FH Key Location/Qualifiers
FT CDS 1. .639
FT /*tag= a
FT /product= "HBc protein"
FT sig_peptide 1. .87
FT /*tag= b
FT mat_peptide 88. .636
FT /*tag= c
FT /product= "Mature HBc protein"
XX
PN WO200177158-A1.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-GB001607.
XX
PR 07-APR-2000; 2000EP-00107118.
XX
PA (MEDE-) MEDEVA EURO LTD.
XX
PI Gehin A, Gilbert R, Stuart D, Rowlands D;
XX
DR WPI; 2002-239995/29.
DR P-PSDB; AAE19793.
XX
PT Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for the
PT prophylactic or therapeutic treatment of humans or animals against e.g.
PT HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-and-
PT mouth disease.
XX
PS Disclosure; Page 23-24; 27pp; English.
XX
CC The present invention relates to hepatitis B virus (HBV) core antigen
CC (HBcAg) fusion proteins and polynucleotides encoding such proteins.
CC Sequences of the invention are useful in methods of prophylactic or
CC therapeutic vaccination or to manufacture medicaments for prophylactic or
CC therapeutic vaccination of the human or animal body against HBV, e.g.
CC against viral hepatitis. They are also useful as a prophylactic vaccine
CC against e.g. hepatitis c virus, influenza, polio, herpes, rabies,
CC acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The
CC present sequence is a DNA encoding hepatitis B virus core antigen (HBcAg)
XX
SQ Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 639;
Best Local Similarity 85.0%; Pred. No. 8.4;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGAUGAUUAGGCAGAGGT 20
||||||:||::||||||||||
Db 33 AGAGATGATTAGGCAGAGGT 14

RESULT 16
ADL56756/c
ID ADL56756 standard; DNA; 646 BP.
XX
AC ADL56756;
XX
DT 17-JUN-2004 (first entry)
XX
DE HBV precore/core DNA.
XX
KW ds; precore/core; cancer; genetic disease; arthritis; AIDS.
XX
OS Hepatitis B virus.
XX
PN US2004063652-A1.
XX
PD 01-APR-2004.
XX
PF 29-MAR-2001; 2001US-00821662.
XX
PR 21-MAR-1988; 88US-00170515.
PR 18-AUG-1989; 89US-00395932.
PR 10-AUG-1990; 90US-00565606.
PR 21-SEP-1990; 90US-00586603.
PR 29-NOV-1991; 91US-00800328.
PR 04-FEB-1992; 92US-00830417.
PR 22-OCT-1992; 92US-00965084.
PR 17-MAR-1993; 93US-00032385.
PR 04-AUG-1993; 93US-00102132.
PR 09-AUG-1993; 93US-00104424.
PR 15-SEP-1993; 93US-00122791.
PR 18-NOV-1993; 93US-00155944.
PR 25-NOV-1997; 97US-00978293.
XX
PA (JOLL/) JOLLY D J.
PA (MONT/) MONTISANO D.
XX
PI Jolly DJ, Montisano D;
XX
DR WPI; 2004-282522/26.
XX
PT Introducing nucleic acid molecules to an animal or human, useful for
PT treating diseases including cancer, genetic diseases, arthritis or AIDS
PT comprises administering a composition comprising two or more gene
PT delivery vehicles.
XX
PS Disclosure; SEQ ID NO 23; 72pp; English.
XX
CC The invention relates to a method of introducing nucleic acid molecules
CC to an animal which comprises administering a composition comprising two
CC or more gene delivery vehicles to an animal at the same time and same
CC site via a single administration device. The method is useful for
CC introducing nucleic acid molecules to an animal, preferably humans for

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CC   treating diseases including cancer, genetic diseases, arthritis or AIDS.
CC   The method can also be administered to plants using traditional methods.
CC   The introduction of multiple or more than one nucleic acid molecule at
CC   one time provide significant advantages because multiple nucleic acid
CC   molecules can provide complementary substances or activities to a single
CC   organ or joint. The difficulty, cost and time to engineer multiple
CC   nucleic acid molecules is much less than engineering a single molecule.
CC   With the use of multiple molecules, there is less chance that one
CC   substance or activity will sterically hinder or otherwise interfere with
CC   another substance or activity. The use of multiple molecules also permits
CC   the expression of different substances or activities from expression
CC   systems subject to differing activating events, thus permitting better
CC   control of differential expression of the different substances or
CC   activities. The present sequence represents the HBV precore/core DNA.
XX
SQ   Sequence 646 BP; 154 A; 170 C; 137 G; 185 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 12;  Length 646;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 17
AAQ47014/c
ID   AAQ47014 standard; DNA; 655 BP.
XX
AC   AAQ47014;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   31-JAN-1994  (first entry)
XX
DE   HBV (adw) corrected precore/core sequence.
XX
KW   Precore; core; coding region; hepatitis B; virus; HBV; plasmid; KSII+;
KW   KSII+HBpc/c; pAM6; deletion; frameshift; PCR; overlap extension; SK+ HBe;
KW   primers; mutation; hepatocellular carcinomas; class-I;
KW   cytotoxic T-lymphocyte; CTL; hepatitis C; infection; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   mutation        334
FT                   /*tag=  a
FT                   /note= "Nucleotide which is deleted in plasmid pAM6"
XX
PN   WO9315207-A2.
XX
PD   05-AUG-1993.
XX
PF   04-FEB-1993;   93WO-US001009.
XX
PR   04-FEB-1992;   92US-00830417.
XX
PA   (VIAG-) VIAGENE INC.
XX
PI   Jolly DJ,  Chang SMW,  Lee WT,  Townsend K,  Odea J;
XX
DR   WPI; 1993-258682/32.
XX
PT   Treatment of hepatitis B and C, and associated carcinoma(s) - using a
PT   vector construct directing the expression of part of hepatitis B or C
PT   antigen.
XX
PS   Example 2; Fig 2; 110pp; English.
XX
CC   This sequence represents the entire precore/core coding region of
CC   hepatitis B virus (HBV) isolated from the plasmid KSII+HBpc/c. This
CC   plasmid was created by ligating a 1.8 kb fragment of plasmid pAM6
CC   containing the entire precore/core region, into the BamHI site of KSII+.
CC   The precore/core region of plasmid KSII+HBpc/p was sequenced and was
CC   found to contain a single base pair deletion which causes a frameshift at
CC   codon 79 which results in two consecutive in-frame TAG codons. This
CC   deletion was corrected by PCR overlap extension in plasmid SK+ HBe using
CC   the primer sequences given in AAQ47015-18 in four separate reactions. The
CC   mutation may also be corrected using the primers given in AAQ47019-23 in
CC   a separate series of reactions. The isolated HBV precore/core region may
CC   be used in a method to induce potent class-I restricted protective and
CC   therapeutic cytotoxic T-lymphocyte (CTL) response, and a humoral response
CC   for the treatment of hepatitis B and C infections, as well as
CC   hepatocellular carcinomas. (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 2;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 18
AAT35649/c
ID   AAT35649 standard; cDNA; 655 BP.
XX
AC   AAT35649;
XX
DT   27-AUG-2003  (revised)
DT   25-FEB-1997  (first entry)
XX
DE   Precore/core region of HBV.
XX
KW   Precore; core region; HBV; hepatitis B virus; gene delivery vehicle; GDV;
KW   immunogen; HBV antigen; hepatitis C carcinoma cell; HBV infection;
KW   gene expression; non-tumourigenic tumour associated antigen; therapy;
KW   altered ras gene; altered p53 gene; altered mucin; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    10. .97
FT                   /*tag=  a
FT                   /note= "precore region"
FT   misc_feature    98. .655
FT                   /*tag=  b
FT                   /note= "core region"
XX
PN   WO9621015-A2.
XX
PD   11-JUL-1996.
XX
PF   22-DEC-1995;   95WO-US016964.
XX
PR   30-DEC-1994;   94US-00368210.
XX
PA   (CHIR ) CHIRON VIAGENE INC.
XX
PI   Jolly DJ,  Montisano D;
XX
DR   WPI; 1996-333990/33.
XX
PT   Introduction of nucleic acid molecules to an animal - comprises
PT   administration of two or more gene delivery vehicles comprising
PT   heterologous nucleic acid.
XX
PS   Disclosure; Page 131; 161pp; English.
XX
CC   This sequence represents the precore/core region of the hepatitis B virus
CC   (HBV) genome. This sequence can be included in a gene delivery vehicle
```

CC (GDV) of the invention, and is used as an immunogenic portion of a HBV
CC antigen. The GDVs can be used in the method of the invention, for
CC introducing nucleic acids into an animal, by administration of a
CC composition comprising two or more GDVs, in combination with a carrier or
CC diluent. Each GDV contains a nucleic acid molecule not naturally
CC contained within the GDV, or directs expression of at least one substance
CC (or biologically active nucleic acid) in host cells containing the GDV.
CC The two GDVs collectively direct the expression of at least two different
CC substances, or direct the expression of at least one substance, where the
CC GDVs differ in one or more biological functions. The GDVs can be used for
CC destroying hepatitis C carcinoma cells, for treating HBV (when a GDV
CC contains an immunogenic HBV fragment such as this sequence). The GDVs can
CC also be used for directing expression of non-tumourigenic, tumour
CC associated antigens (such as altered ras gene), altered p53 gene, and
CC altered mucin. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 655;
Best Local Similarity 85.0%; Pred. No. 8.5;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGAUGAUUAGGCAGAGGT 20
||||||:||::||||||||||
Db 43 AGAGATGATTAGGCAGAGGT 24

RESULT 19
AAH77569/c
ID AAH77569 standard; DNA; 655 BP.
XX
AC AAH77569;
XX
DT 19-OCT-2001 (first entry)
XX
DE HBV genotype G strain US1 preCore/Core DNA.
XX
KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW HBeAg; ds.
XX
OS Hepatitis B virus.
XX
PN WO200140279-A2.
XX
PD 07-JUN-2001.
XX
PF 20-NOV-2000; 2000WO-EP011526.
XX
PR 03-DEC-1999; 99EP-00870252.
PR 07-DEC-1999; 99US-0169287P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Van Geyt C, De Gendt S;
XX
DR WPI; 2001-374785/39.
XX
PT Novel isolated and/or purified hepatitis B virus polypeptide and
PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT therapy.
XX
PS Claim 3; Fig 7; 94pp; English.
XX
CC The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC This genotype was found with a high prevalence in patients chronically
CC infected with HBV and residing in Europe and the USA. The invention
CC relates to a fully defined sequence of 3248 nucleotides as given in
CC specification, a sequence with 92% identity to the given sequence, or
CC sequence that is degenerate to the mentioned sequences. These
CC polynucleotides are useful for HBV genotyping. The proteins encoded by
CC the polynucleotides are useful for detecting antibodies in a biological
CC sample. Ligands that bind to the proteins and antibodies directed against
CC the proteins are useful for detecting the proteins and for detecting
CC HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC preparing a vaccine or medicament for treating HBV infections. The
CC present sequence is provided in an alignment of preCore/Core sequences of
CC an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC US6, US7, US9, US10) of HBV genotype G
XX
SQ Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

Query Match 100.0%; Score 20; DB 4; Length 655;
Best Local Similarity 85.0%; Pred. No. 8.5;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGAUGAUUAGGCAGAGGT 20
||||||:||::||||||||||
Db 33 AGAGATGATTAGGCAGAGGT 14

RESULT 20
AAH77568/c
ID AAH77568 standard; DNA; 655 BP.
XX
AC AAH77568;
XX
DT 19-OCT-2001 (first entry)
XX
DE HBV genotype G strain FR2 preCore/Core DNA.
XX
KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW HBeAg; ds.
XX
OS Hepatitis B virus.
XX
PN WO200140279-A2.
XX
PD 07-JUN-2001.
XX
PF 20-NOV-2000; 2000WO-EP011526.
XX
PR 03-DEC-1999; 99EP-00870252.
PR 07-DEC-1999; 99US-0169287P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Van Geyt C, De Gendt S;
XX
DR WPI; 2001-374785/39.
XX
PT Novel isolated and/or purified hepatitis B virus polypeptide and
PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT therapy.
XX
PS Claim 3; Fig 7; 94pp; English.
XX
CC The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC This genotype was found with a high prevalence in patients chronically
CC infected with HBV and residing in Europe and the USA. The invention
CC relates to a fully defined sequence of 3248 nucleotides as given in
CC specification, a sequence with 92% identity to the given sequence, or
CC sequence that is degenerate to the mentioned sequences. These
CC polynucleotides are useful for HBV genotyping. The proteins encoded by
CC the polynucleotides are useful for detecting antibodies in a biological
CC sample. Ligands that bind to the proteins and antibodies directed against
CC the proteins are useful for detecting the proteins and for detecting
CC HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC preparing a vaccine or medicament for treating HBV infections. The
CC present sequence is provided in an alignment of preCore/Core sequences of
CC an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,

```
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 21
AAH77574/c
ID   AAH77574 standard; DNA; 655 BP.
XX
AC   AAH77574;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US10 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 22
AAH77573/c
ID   AAH77573 standard; DNA; 655 BP.
XX
AC   AAH77573;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US7 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 23
```

```
AAH77570/c
ID   AAH77570 standard; DNA; 655 BP.
XX
AC   AAH77570;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US3 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 24
AAH77571/c
ID   AAH77571 standard; DNA; 655 BP.
XX
AC   AAH77571;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US5 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 655 BP; 138 A; 154 C; 140 G; 195 T; 0 U; 28 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 25
AAD21244/c
ID   AAD21244 standard; DNA; 655 BP.
XX
AC   AAD21244;
XX
DT   15-JAN-2002  (first entry)
XX
DE   Hepatitis B virus adw strain precore/core mutant DNA.
XX
KW   Hepatitis B; hepatitis C; immunogen; HBV; HCV; hepatocellular carcinoma;
KW   HCC; gene therapy; virucide; hepatotropic; antiinflammatory; cytostatic;
KW   mutant; ds.
XX
OS   Hepatitis B virus.
```

```
XX
FH   Key             Location/Qualifiers
FT   misc_feature    11. .97
FT                   /*tag=  a
FT                   /note= "Precore region"
FT   misc_feature    98. .655
FT                   /*tag=  b
FT                   /note= "Core region"
FT   mutation        replace(332. .334, CC)
FT                   /*tag=  c
FT   mutation        replace(338. .340, CAA)
FT                   /*tag=  d
XX
PN   US6297048-B1.
XX
PD   02-OCT-2001.
XX
PF   07-JUN-1995;   95US-00483511.
XX
PR   04-FEB-1992;   92US-00830417.
PR   17-MAR-1993;   93US-00032385.
PR   04-AUG-1993;   93US-00102132.
PR   05-AUG-1994;   94US-00286829.
PR   19-JAN-1995;   95US-00374414.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Chang SMW,  Lee WTL,  Townsend K,  O'dea J;
XX
DR   WPI; 2001-647290/74.
XX
PT   New vectors that direct the (co-)expression of one or more immunogenic
PT   portions of the hepatitis B or C virus antigen(s), useful in gene
PT   therapy, e.g. for treating or preventing hepatitis B or C infections, or
PT   hepatocellular carcinomas.
XX
PS   Example 2; Fig 2; 64pp; English.
XX
CC   The present invention relates to a method for treating hepatitis B or C
CC   infections. The method involves administering a vector construct that
CC   directs the expression of at least one immunogenic portion of hepatitis B
CC   virus (HBV) antigen, containing HBeAg, HbcAg, HbsAg, S, Pre-S1, Pre-S2,
CC   open reading frame (ORF) 5, ORF 6, HBV pol or HBxAg or co-expression of
CC   at least one immunogenic portion of a HBV antigen and at least one
CC   immunogenic portion of a hepatitis C virus (HCV) antigen. The vectors are
CC   useful in gene therapy, particularly for treating or preventing hepatitis
CC   B and hepatitis C infections, as well as hepatocellular carcinomas (HCC).
CC   The present sequence is a PCR primer used for amplifying Hepatitis B
CC   virus adw strain precore/core mutant DNA
XX
SQ   Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 26
ABX80077/c
ID   ABX80077 standard; DNA; 655 BP.
XX
AC   ABX80077;
XX
DT   22-APR-2003  (first entry)
XX
DE   Hepatitis B virus precore/core DNA.
XX
KW   Hepatitis B virus; hepatitis C virus; hepatitis C infection; poliovirus;
KW   hepatitis B infection; hepatitis C antigen; polyprotein antigen; SV40;
KW   rhinovirus; pox virus; canary pox virus; vaccinia virus; influenza virus;
KW   adenovirus; parvovirus; adeno-associated virus; herpes virus; measles;
KW   corona virus; HIV; human immunodeficiency virus; Sindbis virus; virucide;
KW   hepatotropic; ds; precore/core DNA.
XX
OS   Hepatitis B virus.
XX
PN   US2002141974-A1.
XX
PD   03-OCT-2002.
XX
PF   24-JUL-2001; 2001US-00912679.
XX
PR   04-FEB-1992;   92US-00830417.
PR   17-MAR-1993;   93US-00032385.
PR   04-AUG-1993;   93US-00102132.
PR   05-AUG-1994;   94US-00286829.
PR   19-JAN-1995;   95US-00374414.
PR   07-JUN-1995;   95US-00483511.
XX
PA   (JOLL/) JOLLY D J.
PA   (CHAN/) CHANG S M W.
PA   (LEEW/) LEE W T L.
PA   (TOWN/) TOWNSEND K.
PA   (ODEA/) O'DEA J.
XX
PI   Jolly DJ,  Chang SMW,  Lee WTL,  Townsend K,  O'dea J;
XX
DR   WPI; 2003-174125/17.
XX
PT   Treating hepatitis C infections in a warm-blooded animal by administering
PT   a vector construct, which directs the expression of an immunogenic
PT   portion of a hepatitis C antigen, and alternatively, with an
PT   immunomodulatory cofactor.
XX
PS   Example 2; Fig 2; 70pp; English.
XX
CC   The invention relates to a method for treating hepatitis C infections in
CC   a warm-blooded animal comprising administering a vector construct which
CC   directs the expression of at least one immunogenic portion of a hepatitis
CC   C antigen, where an immune response is generated, and alternatively, in
CC   combination with an immunomodulatory cofactor. The invention also relates
CC   to a vector construct which directs the co-expression of at least one
CC   immunogenic portion of a hepatitis B antigen and at least one immunogenic
CC   portion of a hepatitis C antigen, an immunogenic portion of the
CC   polyprotein antigen, or an immunogenic portion of the polyprotein antigen
CC   and an immunoregulatory cofactor. A recombinant virus carrying the vector
CC   construct is selected from poliovirus, rhinovirus, pox virus, canary pox
CC   virus, vaccinia virus, influenza virus, adenovirus, parvovirus, adeno-
CC   associated virus, herpes virus, SV40, HIV, measles, corona virus or
CC   Sindbis virus. This sequence represents hepatitis B virus precore/core
CC   DNA used in the method of the invention
XX
SQ   Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 9;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 27
ABX96938/c
ID   ABX96938 standard; DNA; 655 BP.
XX
AC   ABX96938;
XX
DT   15-MAY-2003  (first entry)
XX
DE   Hepatitis B virus (HBV) DNA.
```

```
XX
KW   Human; HBV; HCV; gene; ds; hepatitis B virus; hepatitis C virus;
KW   intracellular infection; HSV; HIV; viral infection; herpes simplex virus;
KW   human immunodeficiency virus; FIV; feline immunodeficiency virus;
KW   parasitic infection; rickettsia; malaria; leishmaniasis; tuberculosis;
KW   bacterial disease; legionella; chlamydia.
XX
OS   Hepatitis B virus.
XX
PN   US2002165172-A1.
XX
PD   07-NOV-2002.
XX
PF   17-DEC-1999;   99US-00466035.
XX
PR   16-SEP-1997;   97US-00931031.
XX
PA   (SALL/) SALLBERG M.
PA   (MILI/) MILICH D R.
PA   (LEEW/) LEE W T L.
XX
PI   Sallberg M,  Milich DR,  Lee WTL;
XX
DR   WPI; 2003-288144/28.
XX
PT   Treating intracellular infections, e.g. viral, parasitic and bacterial
PT   diseases, comprises administering a vector construct which directs the
PT   expression of an immunogenic portion of an antigen from an intracellular
PT   pathogen.
XX
PS   Disclosure; Page 44-45; 69pp; English.
XX
CC   The invention relates to a method for treating intracellular infections
CC   within warm-blooded animals comprising administering to a warm-blooded
CC   animal a vector construct which directs the expression of at least one
CC   immunogenic portion of an antigen derived from an intracellular pathogen,
CC   and a protein having the immunogenic portion of the antigen to generate
CC   an immune response. The method is useful for treating intracellular
CC   infections or diseases including viral infections (e.g. hepatitis B virus
CC   (HBV), hepatitis C virus (HCV), herpes simplex virus (HSV), human
CC   immunodeficiency virus (HIV) or feline immunodeficiency virus (FIV)),
CC   parasitic infections (e.g. rickettsia, leishmaniasis or malaria) and
CC   certain bacterial diseases (e.g. legionella, tuberculosis or chlamydia).
CC   This sequence represents hepatitis B virus DNA used in the method of the
CC   invention
XX
SQ   Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 10;  Length 655;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         43 AGAGATGATTAGGCAGAGGT 24


RESULT 28
AAN91081/c
ID   AAN91081 standard; DNA; 660 BP.
XX
AC   AAN91081;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1990  (first entry)
XX
DE   DNA sequence of subclones encompassing the core (C) and precore (preC)
DE   antigens (Ag) of an adw serotype hepatitis B (HB) virus.
XX
KW   Hepatitis B virus; core gene; precore gene; antigen; vaccine;
KW   polypeptide expression sequence; AcNPV transfer vector pAcYM1;
KW   pAcYM1KTpc; pAcYM1KTc; recombinant baculovirus; YM1KYpc; MY1KTc.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .658
FT                   /*tag=  e
FT   misc_feature    2. .100
FT                   /*tag=  c
FT                   /note= "This is labelled 'preCore'"
FT   CDS             14. .82
FT                   /*tag=  a
FT                   /product= "Precore antigen"
FT   misc_feature    83. .659
FT                   /*tag=  d
FT                   /note= "This labelled 'Core'"
FT   CDS             101. .658
FT                   /*tag=  b
FT                   /product= "Core Antigen"
FT   conflict        169
FT                   /*tag=  f
FT                   /note= "Differs from the HB virus adw sequence published
FT                   by Ono and associates (1983)"
FT   conflict        181. .182
FT                   /*tag=  g
FT                   /note= "As above"
FT   conflict        217
FT                   /*tag=  h
FT                   /note= "As above"
FT   conflict        274
FT                   /*tag=  i
FT                   /note= "As above"
FT   conflict        329
FT                   /*tag=  j
FT                   /note= "As above"
FT   conflict        346
FT                   /*tag=  k
FT                   /note= "As above"
XX
PN   WO8901518-A.
XX
PD   23-FEB-1989.
XX
PF   11-AUG-1988;   88WO-GB000663.
XX
PR   12-AUG-1987;   87GB-00019108.
PR   12-JUL-1988;   88GB-00016084.
XX
PA   (NATU-) NATURAL ENVIRON RES.
XX
PI   Bishop DH,  Emery VC;
XX
DR   WPI; 1989-068873/09.
DR   P-PSDB; AAP90702.
XX
PT   New plasmid replicon for inserting several genes into vector - contg. two
PT   polypeptide expression structures, and derived viral vectors for
PT   infecting insect cells.
XX
PS   Disclosure; Page ?; 74pp; English.
XX
CC   The coding sequences of the preC and C Ags of HB virus were inserted into
CC   Autograph californica nuclear polyhedrosis virus (AcNPV) transfer vector
CC   pAcYM1. The derived recombinant transfer vectors were called pAcYM1KTpc
CC   and pAcYM1KTc. Following cotransfection with infectious AcNPV DNA,
CC   recombinant baculoviruses were obtained - YM1KYc and YM1KYpc. It was
CC   determined that all the HBcAg and HBpcAg was cell associated and that the
CC   yield of purified HBcAg was of the order of 5 mg per liter of 1x10(9)
CC   infected cells. Such Ag may be useful in vaccines. (Updated on 25-MAR-
CC   2003 to correct PR field.)
XX
SQ   Sequence 660 BP; 156 A; 171 C; 143 G; 189 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 660;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
```

```
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         46 AGAGATGATTAGGCAGAGGT 27


RESULT 29
AAH77572/c
ID   AAH77572 standard; DNA; 664 BP.
XX
AC   AAH77572;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype G strain US6 preCore/Core DNA.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW   HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 3; Fig 7; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an alignment of preCore/Core sequences of
CC   an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC   US6, US7, US9, US10) of HBV genotype G
XX
SQ   Sequence 664 BP; 146 A; 160 C; 144 G; 208 T; 0 U; 6 Other;

  Query Match           100.0%;  Score 20;  DB 4;  Length 664;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 30
ADO07220/c
ID   ADO07220 standard; DNA; 669 BP.
XX
AC   ADO07220;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Hepatitis B virus core antigen DNA.
XX
KW   HBcAg; immunomodulator; vaccine; gene; ss.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             10. .669
FT                   /*tag=  a
FT                   /product= "HBcAg"
FT                   /partial
FT                   /note= "No start codon"
XX
PN   WO2004035007-A2.
XX
PD   29-APR-2004.
XX
PF   17-OCT-2003; 2003WO-US033178.
XX
PR   17-OCT-2002; 2002US-0419279P.
XX
PA   (ORAG-) ORAGEN CORP.
XX
PI   Michaels F;
XX
DR   WPI; 2004-348329/32.
DR   P-PSDB; ADO07221.
XX
PT   Modulating a systemic immune response to a peptide in a mammal comprises
PT   transmucosally administering a macromolecular aggregate of the peptide.
XX
PS   Disclosure; SEQ ID NO 1; 81pp; English.
XX
CC   The present sequence is the DNA sequence of the hepatitis B virus core
CC   antigen (HBcAg) gene from HBV serotype ayw. A peptide comprising a HBV
CC   protein can be used in claimed methods of the invention for modulating an
CC   immune response in a mammal. A method of inducing a systemic immune
CC   response to a peptide in a mammal comprises transmucosally administering
CC   to the mammal a macromolecular aggregate of the peptide. The
CC   macromolecular aggregate comprises at least 10 peptide subunits, may have
CC   a molecular weight of over 1,000 kDa, and is preferably at least 5 nm in
CC   diameter. It is resistant to digestive degradation, being stabilised in
CC   aggregate form by chemical treatment and/or by recombinant protein
CC   engineering of the peptide. The peptide preferably comprises a HBV
CC   protein selected from HBV surface protein, nucleocapsid protein or
CC   envelope protein. Transmucosal administration to a mammal of a
CC   macromolecular aggregate of a HBV surface protein engenders a systemic
CC   immune response in the mammal. A method of suppressing an immune response
CC   in a mammal involves transmucosally administering a monomolecular peptide
CC   that is resistant to digestive degradation and which may be stabilised by
CC   chemical treatment or protein engineering, and which may be derived from
CC   a HBV protein. A monomolecular peptide is useful for the induction of
CC   oral tolerance when induction of systemic immunity is undesirable, e.g.
CC   in cases of chronic infections.
XX
SQ   Sequence 669 BP; 155 A; 170 C; 148 G; 196 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 12;  Length 669;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         63 AGAGATGATTAGGCAGAGGT 44
```

```
RESULT 31
AAD09092/c
ID   AAD09092 standard; DNA; 673 BP.
XX
AC   AAD09092;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Hepatitis B virus FR1 strain genotype G PreCore/HBcAg DNA.
XX
KW   HBV genotype G; precore; HBpol; polymerase; envelope protein; preS1;
KW   preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease;
KW   hepatitis; liver cancer; HBcAg; core antigen; ds.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .672
FT                   /*tag=  a
FT                   /product= "PreCore/HBcAg core protein"
FT                   /transl_except= (pos:4. .6, aa:Xaa)
FT                   /transl_except= (pos:82. .84, aa:Xaa)
FT                   /note= "Xaa corresponds to in-frame stop codon; Does not
FT                   include stop codon"
FT                   /partial
FT   misc_feature    1. .87
FT                   /*tag=  b
FT                   /note= "PreCore protein DNA"
FT   misc_feature    88. .672
FT                   /*tag=  c
FT                   /note= "HBcAg core protein DNA"
FT   misc_feature    94. .129
FT                   /*tag=  d
FT                   /note= "Core insert peptide DNA"
XX
PN   WO200138498-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US032108.
XX
PR   24-NOV-1999;   99US-0167206P.
XX
PA   (PHAR-) PHARMASSET INC.
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Schinazi R,  De Gendt S,  Van Geyt C,  Zoulim F,  Fried M;
PI   Rossau R;
XX
DR   WPI; 2001-367676/38.
DR   P-PSDB; AAE04707.
XX
PT   Novel hepatitis B virus genotype G, nucleic acids encoding virus,
PT   polypeptides encoded by nucleic acids, useful for preparing vaccine to
PT   treat or prevent the hepatitis B virus genotype G infection in a subject.
XX
PS   Claim 4; Page 56-57; 84pp; English.
XX
CC   The present invention relates to hepatitis B virus (HBV) strain FR1,
CC   genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1,
CC   PreS2 and surface antigen HBsAg) and HBX proteins. HBV genotype G nucleic
CC   acids and polypeptides are useful for diagnosing, prognosing and treating
CC   infections caused by HBV genotype G. They can be used in a vaccine to
CC   treat or prevent HBV genotype G infection. The HBV genotype G derived
CC   nucleic acids and antibodies are useful for detecting HBV genotype G in a
CC   sample or diagnosis of HBV genotype G infection. The presence of HBV
CC   genotype G statistically correlates with the presence of liver damage
CC   and/or liver cancer in the subject. The HBV genotype G core insert
CC   peptide encoding nucleic acid is useful for designing monitoring assays
CC   to study and predict the evolution of anti-HBe and anti-HBc antibodies
CC   and HBeAg (genotype G e antigen) in patients infected with HBV. The
CC   antibodies or antigens of HBV genotype G are useful for identifying a
CC   stage of liver disease caused by HBV genotype G. The present sequence is
CC   hepatitis B virus (HBV) strain FR1, genotype G DNA fragment encoding
CC   PreCore/Core antigen (HBcAg) protein
XX
SQ   Sequence 673 BP; 148 A; 165 C; 146 G; 214 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 673;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14


RESULT 32
AAH77563/c
ID   AAH77563 standard; DNA; 675 BP.
XX
AC   AAH77563;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV preCore/Core gene.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBeAg; ds.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Claim 4; Fig 2; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is the complete coding sequence of the HBV preCore/Core
CC   gene
XX
SQ   Sequence 675 BP; 149 A; 165 C; 147 G; 214 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 675;
  Best Local Similarity   85.0%;  Pred. No. 8.5;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14
```

RESULT 33
AAH77566/c
ID AAH77566 standard; DNA; 681 BP.
XX
AC AAH77566;
XX
DT 19-OCT-2001 (first entry)
XX
DE HBV genotype A strain HBVXCPS preCore/Core DNA.
XX
KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW HBeAg; ds.
XX
OS Hepatitis B virus.
XX
PN WO200140279-A2.
XX
PD 07-JUN-2001.
XX
PF 20-NOV-2000; 2000WO-EP011526.
XX
PR 03-DEC-1999; 99EP-00870252.
PR 07-DEC-1999; 99US-0169287P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Van Geyt C, De Gendt S;
XX
DR WPI; 2001-374785/39.
XX
PT Novel isolated and/or purified hepatitis B virus polypeptide and
PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT therapy.
XX
PS Example 2; Fig 7; 94pp; English.
XX
CC The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC This genotype was found with a high prevalence in patients chronically
CC infected with HBV and residing in Europe and the USA. The invention
CC relates to a fully defined sequence of 3248 nucleotides as given in
CC specification, a sequence with 92% identity to the given sequence, or
CC sequence that is degenerate to the mentioned sequences. These
CC polynucleotides are useful for HBV genotyping. The proteins encoded by
CC the polynucleotides are useful for detecting antibodies in a biological
CC sample. Ligands that bind to the proteins and antibodies directed against
CC the proteins are useful for detecting the proteins and for detecting
CC HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC preparing a vaccine or medicament for treating HBV infections. The
CC present sequence is provided in an alignment of preCore/Core sequences of
CC an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC US6, US7, US9, US10) of HBV genotype G
XX
SQ Sequence 681 BP; 151 A; 166 C; 139 G; 189 T; 0 U; 36 Other;

  Query Match   100.0%; Score 20; DB 4; Length 681;
  Best Local Similarity   85.0%; Pred. No. 8.5;
  Matches   17; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14
```

RESULT 34
AAH77567/c
ID AAH77567 standard; DNA; 681 BP.
XX
AC AAH77567;
XX
DT 19-OCT-2001 (first entry)
XX
DE HBV genotype G strain FR1 preCore/Core DNA.
XX
KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
KW HBeAg; ds.
XX
OS Hepatitis B virus.
XX
PN WO200140279-A2.
XX
PD 07-JUN-2001.
XX
PF 20-NOV-2000; 2000WO-EP011526.
XX
PR 03-DEC-1999; 99EP-00870252.
PR 07-DEC-1999; 99US-0169287P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Stuyver L, Van Geyt C, De Gendt S;
XX
DR WPI; 2001-374785/39.
XX
PT Novel isolated and/or purified hepatitis B virus polypeptide and
PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT therapy.
XX
PS Claim 3; Fig 7; 94pp; English.
XX
CC The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC This genotype was found with a high prevalence in patients chronically
CC infected with HBV and residing in Europe and the USA. The invention
CC relates to a fully defined sequence of 3248 nucleotides as given in
CC specification, a sequence with 92% identity to the given sequence, or
CC sequence that is degenerate to the mentioned sequences. These
CC polynucleotides are useful for HBV genotyping. The proteins encoded by
CC the polynucleotides are useful for detecting antibodies in a biological
CC sample. Ligands that bind to the proteins and antibodies directed against
CC the proteins are useful for detecting the proteins and for detecting
CC HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC preparing a vaccine or medicament for treating HBV infections. The
CC present sequence is provided in an alignment of preCore/Core sequences of
CC an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3,
CC US6, US7, US9, US10) of HBV genotype G
XX
SQ Sequence 681 BP; 149 A; 165 C; 147 G; 214 T; 0 U; 6 Other;

  Query Match   100.0%; Score 20; DB 4; Length 681;
  Best Local Similarity   85.0%; Pred. No. 8.5;
  Matches   17; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db         33 AGAGATGATTAGGCAGAGGT 14
```

RESULT 35
AAN80943/c
ID AAN80943 standard; DNA; 750 BP.
XX
AC AAN80943;
XX
DT 25-MAR-2003 (revised)
DT 19-NOV-1990 (first entry)

XX
DE HBV core gene of plasmid pHBV-8.
XX
KW Hepatitis B core antigen; virus; vaccine; immunoassay; ss.
XX
OS Hepatitis B virus.
XX
FH Key Location/Qualifiers
FT CDS 31. .675
FT /*tag= a
FT /product= "HBcAg"
XX
PN EP272483-A.
XX
PD 29-JUN-1988.
XX
PF 25-NOV-1987; 87EP-00117370.
XX
PR 19-DEC-1986; 86US-00944645.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Andersen PR, Mushahwar IK, Mimms LT, Staller JM;
XX
DR WPI; 1988-176639/26.
DR P-PSDB; AAP80961.
XX
PT Polynucleotide encoding HBEAG and HBCAG immuno-reactive polypeptide -
PT useful in immunoassays, for raising antibodies and as vaccine prods.
XX
PS Disclosure; Page ?; 32pp; English.
XX
CC The cloned HBV DNA can be used to engineer plasmids for HBcAg synthesis
CC in bacteria. The DNA may be fused to a gene for beta galactosidase. The
CC recombinant protein can be used for immuno- assays, to raise antibodies,
CC and in vaccines. See also AAN82265 and 66. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 750 BP; 176 A; 192 C; 160 G; 222 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 1; Length 750;
Best Local Similarity 85.0%; Pred. No. 8.6;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGAUGAUUAGGCAGAGGT 20
||||||:||::||||||||||
Db 63 AGAGATGATTAGGCAGAGGT 44

RESULT 36
AAH77169/c
ID AAH77169 standard; DNA; 909 BP.
XX
AC AAH77169;
XX
DT 23-JAN-2002 (first entry)
XX
DE Regulatory and coding region of the X15 component in the X-myc construct.
XX
KW Transgenic mouse; cancer; oncogene; bicistronic hepatitis B virus; HBV;
KW X15-c-myc transgene; hepatocellular carcinoma; malignant liver tumour;
KW X15; c-myc; murine; HBX; carcinogen; ds.
XX
OS Hepatitis B virus.
XX
PN US6274788-B1.
XX
PD 14-AUG-2001.
XX
PF 02-FEB-1999; 99US-00243282.
XX
PR 23-SEP-1998; 98IN-DE002858.
XX
PA (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
PA (NAIM-) NAT INST IMMUNOLOGY.
XX
PI Kumar V, Singh M, Totey S, Anand R;
XX
DR WPI; 2002-009266/01.
XX
PT New bicistronic hepatitis B virus (HBV) X15-c-myc transgene, useful for
PT producing transgenic mouse model systems for human hepatocellular
PT carcinoma, comprises HBV X15 transgene and c-myc transgene.
XX
PS Claim 3; Fig 3; 12pp; English.
XX
CC This polynucleotide represents the sequence of the regulatory and coding
CC regions of the X15 component in the X-myc construct. The invention
CC relates to a bicistronic hepatitis B virus (HBV) X15-c-myc transgene,
CC comprising of the HBV X15 gene and c-myc gene. The myc gene is known to
CC be an activatable oncogene. The transgene encodes a truncated HBV X15
CC protein that has amino acids 58-154 of HBV X15 and a murine c-myc
CC protein, respectively. A transgenic mouse containing the transgene
CC construct is useful for screening a candidate substance (CS), to
CC determine whether CS promotes hepatocellular carcinoma. This is
CC determined by exposing a transgenic mouse to CS, and monitoring the mouse
CC for the development of hepatocellular carcinoma, where an increase in the
CC development of hepatocellular carcinoma in the transgenic mouse exposed
CC to CS compared to the development of hepatocellular carcinoma in a
CC transgenic mouse not exposed to CS, indicates that CS promotes
CC hepatocellular carcinoma. The transgenic mice can be employed as a source
CC for cell and tissue culture. The transgenic animal models comprising of
CC the HBV X15-c-myc transgene for hepatocellular carcinoma are superior to
CC any transgenic animal model system for hepatocellular carcinoma in that
CC the transgenic mice develop more aggressive and accelerated onset of
CC malignant liver tumours in all lobes causing death of the affected
CC animals in 20-22 weeks, that is faster than the time taken by the other
CC transgenic animals to even develop a tumour
XX
SQ Sequence 909 BP; 210 A; 236 C; 211 G; 252 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 909;
Best Local Similarity 85.0%; Pred. No. 8.8;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGAUGAUUAGGCAGAGGT 20
||||||:||::||||||||||
Db 851 AGAGATGATTAGGCAGAGGT 832

RESULT 37
AAV82691/c
ID AAV82691 standard; DNA; 1334 BP.
XX
AC AAV82691;
XX
DT 16-FEB-1999 (first entry)
XX
DE Fulminant hepatitis B virus genotype D variant FHBV12 sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;

```
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1334 BP; 288 A; 363 C; 311 G; 372 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1334;
  Best Local Similarity   85.0%;  Pred. No. 9.2;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        735 AGAGATGATTAGGCAGAGGT 716


RESULT 38
AAV82688/c
ID   AAV82688 standard; DNA; 1395 BP.
XX
AC   AAV82688;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV5 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1395 BP; 277 A; 387 C; 331 G; 398 T; 0 U; 2 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1395;
  Best Local Similarity   85.0%;  Pred. No. 9.2;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 39
AAV82687/c
ID   AAV82687 standard; DNA; 1400 BP.
XX
AC   AAV82687;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV4 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
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CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1400 BP; 287 A; 388 C; 332 G; 393 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1400;
  Best Local Similarity   85.0%;  Pred. No. 9.2;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 40
AAV82692/c
ID   AAV82692 standard; DNA; 1445 BP.
XX
AC   AAV82692;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV13 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1445 BP; 297 A; 406 C; 338 G; 404 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1445;
  Best Local Similarity   85.0%;  Pred. No. 9.2;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 41
AAV82685/c
ID   AAV82685 standard; DNA; 1445 BP.
XX
AC   AAV82685;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV2 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1445 BP; 298 A; 393 C; 340 G; 414 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1445;
  Best Local Similarity   85.0%;  Pred. No. 9.2;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 42
AAV82690/c
ID   AAV82690 standard; DNA; 1445 BP.
XX
AC   AAV82690;
XX
DT   16-FEB-1999  (first entry)
XX
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DE   Fulminant hepatitis B virus genotype D variant FHBV7 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1445 BP; 293 A; 402 C; 340 G; 410 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1445;
  Best Local Similarity   85.0%;  Pred. No. 9.2;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 43
AAV82684/c
ID   AAV82684 standard; DNA; 1445 BP.
XX
AC   AAV82684;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV1 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1445 BP; 298 A; 400 C; 336 G; 411 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1445;
  Best Local Similarity   85.0%;  Pred. No. 9.2;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 44
AAV82695/c
ID   AAV82695 standard; DNA; 1500 BP.
XX
AC   AAV82695;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant CHBV2 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
```

PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1500 BP; 308 A; 412 C; 347 G; 433 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1500;
Best Local Similarity 85.0%; Pred. No. 9.3;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGAUGAUUAGGCAGAGGT 20
||||:||::||||||||||
Db 846 AGAGATGATTAGGCAGAGGT 827

RESULT 45
AAV82683/c
ID AAV82683 standard; DNA; 1500 BP.
XX
AC AAV82683;
XX
DT 16-FEB-1999 (first entry)
XX
DE Fulminant hepatitis B virus genotype D variant AHBV1 sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations
PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1500 BP; 305 A; 411 C; 354 G; 430 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1500;
Best Local Similarity 85.0%; Pred. No. 9.3;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGAUGAUUAGGCAGAGGT 20
||||:||::||||||||||
Db 846 AGAGATGATTAGGCAGAGGT 827

RESULT 46
AAV82694/c
ID AAV82694 standard; DNA; 1500 BP.
XX
AC AAV82694;
XX
DT 16-FEB-1999 (first entry)
XX
DE Fulminant hepatitis B virus genotype D variant HBVP2CSX sequence.
XX
KW Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW HBV-related disease; ss.
XX
OS Hepatitis B virus.
XX
PN WO9845421-A2.
XX
PD 15-OCT-1998.
XX
PF 08-APR-1998; 98WO-EP002048.
XX
PR 09-APR-1997; 97GB-00007221.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Carman B;
XX
DR WPI; 1999-009329/01.
XX
PT New hepatitis B virus nucleic acid with combination of specific mutations
PT - useful for, e.g. detection of binding interactions between host or
PT viral proteins and HBV nucleic.
XX
PS Disclosure; Fig 5; 85pp; English.
XX
CC The present sequence represents part of the genome of a fulminant
CC Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC a mutation (i.e. alteration from the normal nucleotide in any of the
CC genotypes A to F) in at least two of the enhancer I region, the negative
CC regulatory element region, the enhancer II/ core upstream regulatory
CC sequence/ basal core promoter region, or a mutation which leads to an X-
CC peptide amino acid change to Cys or Met. The HBV variants of the
CC invention are used to detect binding interactions between host or viral
CC proteins and HBV nucleic acid. Probes that hybridise to any of the
CC specified mutated regions are used to detect HBV-related disease,
CC especially fulminant infection, but also severe chronic infection or
CC serologically unusual forms of disease. Combinations of the specified
CC mutations are associated with fulminant infections, probably because they
CC reduce the ability to bind inhibitory proteins in the host cell
XX
SQ Sequence 1500 BP; 305 A; 408 C; 349 G; 438 T; 0 U; 0 Other;

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  Query Match             100.0%;  Score 20;  DB 2;  Length 1500;
  Best Local Similarity   85.0%;  Pred. No. 9.3;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 47
AAV82686/c
ID   AAV82686 standard; DNA; 1500 BP.
XX
AC   AAV82686;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV3 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1500 BP; 305 A; 413 C; 353 G; 429 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1500;
  Best Local Similarity   85.0%;  Pred. No. 9.3;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 48
AAV82706/c
ID   AAV82706 standard; DNA; 1500 BP.
XX
AC   AAV82706;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Wild type hepatitis B virus genotype D nucleotides 1000-2500.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of wild type Hepatitis
CC   B virus genotype D, nucleotides 1000 to 2500. Mutations occur in this
CC   region in fulminant hepatitis B virus (FHBV) patients. The specification
CC   describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e.
CC   alteration from the normal nucleotide in any of the genotypes A to F) in
CC   at least two of the enhancer I region, the negative regulatory element
CC   region, the enhancer II/ core upstream regulatory sequence/ basal core
CC   promoter region, or a mutation which leads to an X-peptide amino acid
CC   change to Cys or Met. The HBV variants of the invention are used to
CC   detect binding interactions between host or viral proteins and HBV
CC   nucleic acid. Probes that hybridise to any of the specified mutated
CC   regions are used to detect HBV-related disease, especially fulminant
CC   infection, but also severe chronic infection or serologically unusual
CC   forms of disease. Combinations of the specified mutations are associated
CC   with fulminant infections, probably because they reduce the ability to
CC   bind inhibitory proteins in the host cell
XX
SQ   Sequence 1500 BP; 304 A; 409 C; 351 G; 436 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1500;
  Best Local Similarity   85.0%;  Pred. No. 9.3;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 49
AAV82689/c
ID   AAV82689 standard; DNA; 1500 BP.
XX
AC   AAV82689;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant FHBV6 sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
```

```
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence rèpresents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1500 BP; 302 A; 416 C; 353 G; 427 T; 0 U; 2 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1500;
  Best Local Similarity   85.0%;  Pred. No. 9.3;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


RESULT 50
AAV82693/c
ID   AAV82693 standard; DNA; 1500 BP.
XX
AC   AAV82693;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fulminant hepatitis B virus genotype D variant HBVP3CSX sequence.
XX
KW   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
KW   HBV-related disease; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO9845421-A2.
XX
PD   15-OCT-1998.
XX
PF   08-APR-1998;   98WO-EP002048.
XX
PR   09-APR-1997;   97GB-00007221.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Carman B;
XX
DR   WPI; 1999-009329/01.
XX
PT   New hepatitis B virus nucleic acid with combination of specific mutations
PT   - useful for, e.g. detection of binding interactions between host or
PT   viral proteins and HBV nucleic.
XX
PS   Disclosure; Fig 5; 85pp; English.
XX
CC   The present sequence represents part of the genome of a fulminant
CC   Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
CC   The specification describes Hepatitis B virus (HBV) nucleic acid that has
CC   a mutation (i.e. alteration from the normal nucleotide in any of the
CC   genotypes A to F) in at least two of the enhancer I region, the negative
CC   regulatory element region, the enhancer II/ core upstream regulatory
CC   sequence/ basal core promoter region, or a mutation which leads to an X-
CC   peptide amino acid change to Cys or Met. The HBV variants of the
CC   invention are used to detect binding interactions between host or viral
CC   proteins and HBV nucleic acid. Probes that hybridise to any of the
CC   specified mutated regions are used to detect HBV-related disease,
CC   especially fulminant infection, but also severe chronic infection or
CC   serologically unusual forms of disease. Combinations of the specified
CC   mutations are associated with fulminant infections, probably because they
CC   reduce the ability to bind inhibitory proteins in the host cell
XX
SQ   Sequence 1500 BP; 314 A; 403 C; 343 G; 440 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 2;  Length 1500;
  Best Local Similarity   85.0%;  Pred. No. 9.3;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGAUGAUUAGGCAGAGGT 20
              |||||:||::||||||||||
Db        846 AGAGATGATTAGGCAGAGGT 827


Search completed: December 15, 2004, 15:38:58
Job time : 182 secs
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